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SEQUENCE LISTING

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Stallings, William C.

<120> GLYPHOSATE TOLERANT 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES

<130> 11899.0175.CNUS01 MOBT:175-2

<140> 09/464,099

<141> 1999-12-16

<150> US 09/137,440

<151> 1998-08-20

<150> US 08/833,485

<151> 1997-04-07

<150> US 08/306,063

<151> 1994-09-13

<150> US 07/749,611

<151> 1991-08-28

<150> US 07/576,537

<151> 1990-08-31

<160> 70

<170> PatentIn version 3.0

<210> 1

<211> 597

<212> DNA

<213> Figwort mosaic virus

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aggaagaatt cttagtccaa agcctcaaca aggtcagggt acagagtctc caaaccatta 180

gccaaaagct acaggagatc aatgaagaat cttcaatcaa agtaaactac tgttccagca 240

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gcatctttga aagtaattct gtcaacatcg agcagctggc ttgtggggac cagacaaaaa 360

aggaatgggtg cagaattggt aggcgcacct accaaaagca tctttgcctt tattgcaaag 420

ataaagcaga ttcctctagt acaagtgggg aacaaaataa cgtggaaaag agctgtcctg 480

108

F

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<213> Agrobacterium sp.

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Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser His

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cgg tcc ttc atg ttc ggc ggt ctc gcg agc ggt gaa acg cgc atc acc 205

Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr

35 40 45

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50 55 60

gcc atg ggc gcc agg atc cgt aag gaa ggc gac acc tgg atc atc gat 301

Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile Asp

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Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp Phe

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ggc aat gcc gcc acg ggc tgc cgc ctg acc atg ggc ctc gtc ggg gtc 397

Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly Val

100 105 110

tac gat ttc gac agc acc ttc atc ggc gac gcc tcg ctc aca aag cgc 445

Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys Arg

115 120 125

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Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val

130 135 140

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Thr Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val	
165 170 175	
aag tcc gcc gtg ctg ctc gcc ggc ctc aac acg ccc ggc atc acg acg	637
Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr Thr	
180 185 190	
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Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu Gln	
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acc atc cgc ctg gaa ggc cgc ggc aag ctc acc ggc caa gtc atc gac	781
Thr Ile Arg Leu Glu Gly Arg Gly Lys Leu Thr Gly Gln Val Ile Asp	
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Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu	
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Leu Val Pro Gly Ser Asp Val Thr Ile Leu Asn Val Leu Met Asn Pro	
260 265 270	
acc cgc acc ggc ctc atc ctg acg ctg cag gaa atg ggc gcc gac atc	925
Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile	
275 280 285	
gaa gtc atc aac ccg cgc ctt gcc ggc ggc gaa gac gtg gcg gac ctg	973
Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu	
290 295 300	
cgc gtt cgc tcc tcc acg ctg aag ggc gtc acg gtg ccg gaa gac cgc	1021
Arg Val Arg Ser Ser Thr Leu Lys Gly Val Thr Val Pro Glu Asp Arg	
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Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala Ala	
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Phe Ala Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg Val	
340 345 350	
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Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu Asn	

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cct gac ggc aag ggg ctc ggc aac gcc tcg ggc gcc gcc gtc gcc acc			1261
Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala Thr			
385	390	395	400
cat ctc gat cac cgc atc gcc atg agc ttc ctc gtc atg ggc ctc gtg			1309
His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Val			
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tcg gaa aac cct gtc acg gtg gac gat gcc acg atg atc gcc acg agc			1357
Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr Ser			
420	425	430	
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Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile Glu			
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ctc tcc gat acg aag gct gcc tgatgacctt cacaatcgcc atcgatggtc			1456
Leu Ser Asp Thr Lys Ala Ala			
450	455		
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gcgggttggc cgattacggg acgatectcg aggatatccg ccgccgcgac gagcgggaca			1936
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Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr
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50 55 60

Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile Asp
65 70 75 80

Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp Phe
85 90 95

Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly Val
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Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys Arg
115 120 125

Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
130 135 140

Lys Ser Glu Asp Gly Asp Arg Leu Pro Val Thr Leu Arg Gly Pro Lys
145 150 155 160

Thr Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
165 170 175

Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr Thr
180 185 190

Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
195 200 205

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210 215 220

Thr Ile Arg Leu Glu Gly Arg Gly Lys Leu Thr Gly Gln Val Ile Asp
 225 230 235 240

Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu
 245 250 255

Leu Val Pro Gly Ser Asp Val Thr Ile Leu Asn Val Leu Met Asn Pro
 260 265 270

Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile
 275 280 285

Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
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Arg Val Arg Ser Ser Thr Leu Lys Gly Val Thr Val Pro Glu Asp Arg
 305 310 315 320

Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala Ala
 325 330 335

Phe Ala Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg Val
 340 345 350

Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu Asn
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Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly Arg
 370 375 380

Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala Thr
 385 390 395 400

His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Val
 405 410 415

Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr Ser
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 435 440 445

113

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Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg Ile Pro
10 15 20 25

ggc gac aag tcc atc tcg cat cgc tcc ttc atg ttt ggc ggt ctc gca 208
Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly Leu Ala
30 35 40

tcg ggc gaa acc cgc atc acc ggc ctt ctg gaa ggc gag gac gtc atc 256
Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp Val Ile
45 50 55

aat aca ggc cgc gcc atg cag gcc atg ggc gcg aaa atc cgt aaa gag 304
Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg Lys Glu
60 65 70

ggc gat gtc tgg atc atc aac ggc gtc ggc aat ggc tgc ctg ttg cag 352
Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu Leu Gln
75 80 85

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Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala Arg Leu
90 95 100 105

acc atg ggc ctt gtc ggc acc tat gac atg aag acc tcc ttt atc ggc 448
Thr Met Gly Leu Val Gly Thr Tyr Asp Met Lys Thr Ser Phe Ile Gly
110 115 120

gac gcc tcg ctg tcg aag cgc ccg atg ggc cgc gtg ctg aac ccg ttg 496
Asp Ala Ser Leu Ser Lys Arg Pro Met Gly Arg Val Leu Asn Pro Leu
125 130 135

114

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ccg atg gcc tcc gcg cag gta aaa tcc gcc gtg ctg ctc gcc ggt ctc Pro Met Ala Ser Ala Gln Val Lys Ser Ala Val Leu Leu Ala Gly Leu 170 175 180 185	640
aac acg ccg ggc gtc acc acc gtc atc gag ccg gtc atg acc cgc gac Asn Thr Pro Gly Val Thr Thr Val Ile Glu Pro Val Met Thr Arg Asp 190 195 200	688
cac acc gaa aag atg ctg cag ggc ttt ggc gcc gac ctc acg gtc gag His Thr Glu Lys Met Leu Gln Gly Phe Gly Ala Asp Leu Thr Val Glu 205 210 215	736
acc gac aag gat ggc gtg cgc cat atc cgc atc acc ggc cag ggc aag Thr Asp Lys Asp Gly Val Arg His Ile Arg Ile Thr Gly Gln Gly Lys 220 225 230	784
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100 105 110

Tyr Asp Met Lys Thr Ser Phe Ile Gly Asp Ala Ser Leu Ser Lys Arg
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Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
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Glu Ala Ala Asp Gly Asp Arg Met Pro Leu Thr Leu Ile Gly Pro Lys
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Thr Ala Asn Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
165 170 175

Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Val Thr Thr
180 185 190

Val Ile Glu Pro Val Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
195 200 205

Gly Phe Gly Ala Asp Leu Thr Val Glu Thr Asp Lys Asp Gly Val Arg
210 215 220

His Ile Arg Ile Thr Gly Gln Gly Lys Leu Val Gly Gln Thr Ile Asp
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Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu
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Leu Val Glu Gly Ser Asp Val Thr Ile Arg Asn Val Leu Met Asn Pro
260 265 270

10
M

F

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 275 280 285

Glu Val Leu Asn Ala Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
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Arg Val Arg Ala Ser Lys Leu Lys Gly Val Val Val Pro Pro Glu Arg
 305 310 315 320

Ala Pro Ser Met Ile Asp Glu Tyr Pro Val Leu Ala Ile Ala Ala Ser
 325 330 335

Phe Ala Glu Gly Glu Thr Val Met Asp Gly Leu Asp Glu Leu Arg Val
 340 345 350

Lys Glu Ser Asp Arg Leu Ala Ala Val Ala Arg Gly Leu Glu Ala Asn
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Gly Val Asp Cys Thr Glu Gly Glu Met Ser Leu Thr Val Arg Gly Arg
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Pro Asp Gly Lys Gly Leu Gly Gly Gly Thr Val Ala Thr His Leu Asp
 385 390 395 400

His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Ala Ala Glu Lys
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Leu

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 <213> Pseudomonas sp.

<222> (34) .. (1380)

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      10              15              20

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Ile Pro Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly
25 30 35

ctc gca tgc ggc gaa acc cgc atc acc ggc ctt ctg gaa ggc gag gac 198
Leu Ala Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp
40 45 50 55

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gtc atc aat aca ggc cgc gcc atg cag gcc atg ggc gcg aaa atc cgt      246
Val Ile Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg
           60                      65                      70

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Leu Gln Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala
90 95 100

cgc ctc acc atg ggc ctt gtc ggc acc tat gac atg aag acc tcc ttt 390
 Arg Leu Thr Met Gly Leu Val Gly Thr Tyr Asp Met Lys Thr Ser Phe
 105 110 115

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Ile Gly Asp Ala Ser Leu Ser Lys Arg Pro Met Gly Arg Val Leu Asn
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Pro Leu Arg Glu Met Gly Val Gln Val Glu Ala Ala Asp Gly Asp Arg
140 145 150

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Met Pro Leu Thr Leu Ile Gly Pro Lys Thr Ala Asn Pro Ile Thr Tyr
155 160 165

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Arg Val Pro Met Ala Ser Ala Gln Val Lys Ser Ala Val Leu Leu Ala
170 175 180

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Gly Leu Asn Thr Pro Gly Val Thr Thr Val Ile Glu Pro Val Met Thr	
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Arg Asp His Thr Glu Lys Met Leu Gln Gly Phe Gly Ala Asp Leu Thr	
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Val Glu Thr Asp Lys Asp Gly Val Arg His Ile Arg Ile Thr Gly Gln	
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Gly Lys Leu Val Gly Gln Thr Ile Asp Val Pro Gly Asp Pro Ser Ser	
235 240 245	
acc gcc ttc ccg ctc gtt gcc gcc ctt ctg gtg gaa ggt tcc gac gtc	822
Thr Ala Phe Pro Leu Val Ala Ala Leu Leu Val Glu Gly Ser Asp Val	
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Thr Ile Arg Asn Val Leu Met Asn Pro Thr Arg Thr Gly Leu Ile Leu	
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Thr Leu Gln Glu Met Gly Ala Asp Ile Glu Val Leu Asn Ala Arg Leu	
280 285 290 295	
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Ala Gly Gly Glu Asp Val Ala Asp Leu Arg Val Arg Ala Ser Lys Leu	
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Lys Gly Val Val Val Pro Pro Glu Arg Ala Pro Ser Met Ile Asp Glu	
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Tyr Pro Val Leu Ala Ile Ala Ala Ser Phe Ala Glu Gly Glu Thr Val	
330 335 340	
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Ala Val Ala Arg Gly Leu Glu Ala Asn Gly Val Asp Cys Thr Glu Gly	
360 365 370 375	
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Glu Met Ser Leu Thr Val Arg Gly Arg Pro Asp Gly Lys Gly Leu Gly	
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395	400	405	
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aac atg atc gcc acg tcc ttc ccc gaa ttc atg gac atg atg ccg gga			1350
Asn Met Ile Ala Thr Ser Phe Pro Glu Phe Met Asp Met Met Pro Gly			
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Leu Gly Ala Lys Ile Glu Leu Ser Ile Leu			
440	445		
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 <213> Pseudomonas sp.

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35 40 45

Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Arg Ala Met Gln
50 55 60

Ala Met Gly Ala Lys Ile Arg Lys Glu Gly Asp Val Trp Ile Ile Asn
65 70 75 80

Gly Val Gly Asn Gly Cys Leu Leu Gln Pro Glu Ala Ala Leu Asp Phe
85 90 95

Gly Asn Ala Gly Thr Gly Ala Arg Leu Thr Met Gly Leu Val Gly Thr
100 105 110

121

F

Tyr Asp Met Lys Thr Ser Phe Ile Gly Asp Ala Ser Leu Ser Lys Arg
115 120 125

Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
130 135 140

Glu Ala Ala Asp Gly Asp Arg Met Pro Leu Thr Leu Ile Gly Pro Lys
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Thr Ala Asn Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
165 170 175

Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Val Thr Thr
180 185 190

Val Ile Glu Pro Val Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
195 200 205

Gly Phe Gly Ala Asp Leu Thr Val Glu Thr Asp Lys Asp Gly Val Arg
210 215 220

His Ile Arg Ile Thr Gly Gln Gly Lys Leu Val Gly Gln Thr Ile Asp
225 230 235 240

Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu
245 250 255

Leu Val Glu Gly Ser Asp Val Thr Ile Arg Asn Val Leu Met Asn Pro
260 265 270

Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile
275 280 285

Glu Val Leu Asn Ala Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
290 295 300

Arg Val Arg Ala Ser Lys Leu Lys Gly Val Val Val Pro Pro Glu Arg
305 310 315 320

Ala Pro Ser Met Ile Asp Glu Tyr Pro Val Leu Ala Ile Ala Ala Ser
325 330 335

Phe Ala Glu Gly Glu Thr Val Met Asp Gly Leu Asp Glu Leu Arg Val
 340 345 350

Lys Glu Ser Asp Arg Leu Ala Ala Val Ala Arg Gly Leu Glu Ala Asn
 355 360 365

Gly Val Asp Cys Thr Glu Gly Glu Met Ser Leu Thr Val Arg Gly Arg
 370 375 380

Pro Asp Gly Lys Gly Leu Gly Gly Gly Thr Val Ala Thr His Leu Asp
 385 390 395 400

His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Ala Ala Glu Lys
 405 410 415

Pro Val Thr Val Asp Asp Ser Asn Met Ile Ala Thr Ser Phe Pro Glu
 420 425 430

Phe Met Asp Met Met Pro Gly Leu Gly Ala Lys Ile Glu Leu Ser Ile
 435 440 445

Leu

<210> 8
 <211> 423
 <212> PRT
 <213> Escherichia coli

<400> 8

Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Thr Ile Asn Leu
 1 5 10 15

Pro Gly Ser Lys Thr Val Ser Asn Arg Ala Leu Leu Leu Ala Ala Leu
 20 25 30

Ala His Gly Lys Thr Val Leu Thr Asn Leu Leu Asp Ser Asp Asp Val
 35 40 45

Arg His Met Leu Asn Ala Leu Thr Ala Leu Gly Val Ser Tyr Thr Leu
 50 55 60

Ser Ala Asp Arg Thr Arg Cys Glu Ile Ile Gly Asn Gly Gly Pro Leu

65					70						75				80
His	Ala	Glu	Gly	Ala	Leu	Glu	Leu	Phe	Leu	Gly	Asn	Ala	Gly	Thr	Ala
				85					90					95	
Met	Arg	Pro	Leu	Ala	Ala	Ala	Leu	Cys	Leu	Gly	Ser	Asn	Asp	Ile	Val
			100					105					110		
Leu	Thr	Gly	Glu	Pro	Arg	Met	Lys	Glu	Arg	Pro	Ile	Gly	His	Leu	Val
		115					120					125			
Asp	Ala	Leu	Arg	Leu	Gly	Gly	Ala	Lys	Ile	Thr	Tyr	Leu	Glu	Gln	Glu
	130					135					140				
Asn	Tyr	Pro	Pro	Leu	Arg	Leu	Gln	Gly	Gly	Phe	Thr	Gly	Gly	Asn	Val
145					150					155				160	
Asp	Val	Asp	Gly	Ser	Val	Ser	Ser	Gln	Phe	Leu	Thr	Ala	Leu	Leu	Met
				165					170					175	
Thr	Ala	Pro	Leu	Ala	Pro	Glu	Asp	Thr	Val	Ile	Arg	Ile	Lys	Gly	Asp
			180					185					190		
Leu	Val	Ser	Lys	Pro	Tyr	Ile	Asp	Ile	Thr	Leu	Asn	Leu	Met	Lys	Thr
	195						200					205			
Phe	Gly	Val	Glu	Ile	Glu	Asn	Gln	His	Tyr	Gln	Gln	Phe	Val	Val	Lys
	210					215					220				
Gly	Gly	Gln	Ser	Tyr	Gln	Ser	Pro	Gly	Thr	Tyr	Leu	Val	Glu	Gly	Asp
225					230					235					240
Ala	Ser	Ser	Ala	Ser	Tyr	Phe	Leu	Ala	Ala	Ala	Ala	Ile	Lys	Gly	Gly
				245					250					255	
Thr	Val	Lys	Val	Thr	Gly	Ile	Gly	Arg	Asn	Ser	Met	Gln	Gly	Asp	Ile
			260					265					270		
Arg	Phe	Ala	Asp	Val	Leu	Glu	Lys	Met	Gly	Ala	Thr	Ile	Cys	Trp	Gly
	275						280					285			
Asp	Asp	Tyr	Ile	Ser	Cys	Thr	Arg	Gly	Glu	Leu	Asn	Ala	Ile	Asp	Met
	290					295					300				
Asp	Met	Asn	His	Ile	Pro	Asp	Ala	Ala	Met	Thr	Ile	Ala	Thr	Ala	Ala
305					310					315				320	
Leu	Phe	Ala	Lys	Gly	Thr	Thr	Arg	Leu	Arg	Asn	Ile	Tyr	Asn	Trp	Arg
				325					330					335	
Val	Lys	Glu	Thr	Asp	Arg	Leu	Phe	Ala	Met	Ala	Thr	Glu	Leu	Arg	Lys
			340					345					350		
Val	Gly	Ala	Glu	Val	Glu	Glu	Gly	His	Asp	Tyr	Ile	Arg	Ile	Thr	Pro

17
124

F

355

360

365

Pro Glu Lys Leu Asn Phe Ala Glu Ile Ala Thr Tyr Asn Asp His Arg
 370 375 380

Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro Val Thr
 385 390 395 400

Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr Phe Glu
 405 410 415

Gln Leu Ala Arg Ile Ser Gln
 420

<210> 9

<211> 1377

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic

<400> 9

ccatggctca cgggtgcaagc agccgtccag caactgctcg taagtctctt ggtctttctg 60
 gaaccgtccg tattccaggt gacaagtcta tctcccacag gtccttcatg tttggaggtc 120
 tcgctagcgg tgaaactcgt atcaccggtc ttttggaagg tgaagatggt atcaacactg 180
 gtaaggctat gcaagctatg ggtgccagaa tccgtaagga aggtgatact tggatcattg 240
 atgggtgttg taacgggtga ctccttgctc ctgaggctcc tctcgatttc ggtaacgctg 300
 caactggttg ccgtttgact atgggtcttg ttgggtgttta cgatttcgat agcactttca 360
 ttgggtgacgc ttctctcact aagcgtccaa tgggtcgtgt gttgaacca cttcgcgaaa 420
 tgggtgtgca ggtgaagtct gaagacgggtg atcgtcttcc agttacctg cgtggaccaa 480
 agactccaac gccaatcacc tacagggtac ctatggcttc cgtcaagtg aagtccgctg 540
 ttctgcttgc tgggtctcaac accccaggta tcaccactgt tatcgagcca atcatgactc 600
 gtgaccacac tgaaaagatg cttcaagggt ttgggtgctaa ccttaccgtt gagactgatg 660
 ctgacgggtg gcgtaccatc cgtcttgaag gtcgtggtaa gctcaccggt caagtgattg 720
 atgttccagg tgatccatcc tctactgctt tcccattggt tgctgccttg cttgttccag 780
 gttccgacgt caccatcctt aacgttttga tgaaccaaac ccgtactggg ctcactttga 840
 ctctgcagga aatgggtgcc gacatcgaag tgatcaaccc acgtcttgct ggtggagaag 900
 acgtggctga cttgcgtggt cgttcttcta ctttgaaggg tgttactggt ccagaagacc 960

gtgctccttc tatgatcgac gagtatccaa ttctcgtgtg tgcagctgca ttcgctgaag 1020
 gtgctaccgt tatgaacggt ttggaagaac tccgtgttaa ggaaagcgac cgtctttctg 1080
 ctgtcgcaaaa cgggtctcaag ctcaacggtg ttgattgcga tgaagggtgag acttctctcg 1140
 tcgtgcgtgg tcgtcctgac ggtaagggtc tcggtaacgc ttctggagca gctgtcgtc 1200
 cccacctcga tcaccgtatc gctatgagct tcctcgttat gggctctcgtt tctgaaaacc 1260
 ctgttactgt tgatgatgct actatgatcg ctactagctt cccagagttc atggatttga 1320
 tggctggtct tggagctaag atcgaactct ccgacactaa ggctgcttga tgagctc 1377

<210> 10
 <211> 318
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (87) .. (317)

<400> 10
 agatctatcg ataagcttga tgtaattgga ggaagatcaa aattttcaat cccattctt 60
 cgattgcttc aattgaagtt tctccg atg gcg caa gtt agc aga atc tgc aat 113
 Met Ala Gln Val Ser Arg Ile Cys Asn
 1 5
 ggt gtg cag aac cca tct ctt atc tcc aat ctg tgc aaa tcc agt caa 161
 Gly Val Gln Asn Pro Ser Leu Ile Ser Asn Leu Ser Lys Ser Ser Gln
 10 15 20 25
 cgc aaa tct ccc tta tgc gtt tct ctg aag acg cag cag cat cca cga 209
 Arg Lys Ser Pro Leu Ser Val Ser Leu Lys Thr Gln Gln His Pro Arg
 30 35 40
 gct tat ccg att tgc tgc tgc tgg gga ttg aag aag agt ggg atg acg 257
 Ala Tyr Pro Ile Ser Ser Ser Trp Gly Leu Lys Lys Ser Gly Met Thr
 45 50 55
 tta att ggc tct gag ctt cgt cct ctt aag gtc atg tct tct gtt tcc 305
 Leu Ile Gly Ser Glu Leu Arg Pro Leu Lys Val Met Ser Ser Val Ser
 60 65 70
 acg gcg tgc atg c 318
 Thr Ala Cys Met
 75

<210> 11

<211> 77
 <212> PRT
 <213> Arabidopsis thaliana

<400> 11

Met Ala Gln Val Ser Arg Ile Cys Asn Gly Val Gln Asn Pro Ser Leu
 1 5 10 15

Ile Ser Asn Leu Ser Lys Ser Ser Gln Arg Lys Ser Pro Leu Ser Val
 20 25 30

Ser Leu Lys Thr Gln Gln His Pro Arg Ala Tyr Pro Ile Ser Ser Ser
 35 40 45

Trp Gly Leu Lys Lys Ser Gly Met Thr Leu Ile Gly Ser Glu Leu Arg
 50 55 60

Pro Leu Lys Val Met Ser Ser Val Ser Thr Ala Cys Met
 65 70 75

<210> 12
 <211> 402
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (87) .. (401)

<400> 12

agatctatcg ataagcttga tgtaattgga ggaagatcaa aattttcaat cccattctt 60

cgattgcttc aattgaagtt tctccg atg gcg caa gtt agc aga atc tgc aat 113
 Met Ala Gln Val Ser Arg Ile Cys Asn
 1 5

ggt gtg cag aac cca tct ctt atc tcc aat ctc tcg aaa tcc agt caa 161
 Gly Val Gln Asn Pro Ser Leu Ile Ser Asn Leu Ser Lys Ser Ser Gln
 10 15 20 25

cgc aaa tct ccc tta tcg gtt tct ctg aag acg cag cag cat cca cga 209
 Arg Lys Ser Pro Leu Ser Val Ser Leu Lys Thr Gln Gln His Pro Arg
 30 35 40

gct tat ccg att tcg tcg tcg tgg gga ttg aag aag agt ggg atg acg 257
 Ala Tyr Pro Ile Ser Ser Ser Trp Gly Leu Lys Lys Ser Gly Met Thr
 45 50 55

tta att ggc tct gag ctt cgt cct ctt aag gtc atg tct tct gtt tcc 305
 Leu Ile Gly Ser Glu Leu Arg Pro Leu Lys Val Met Ser Ser Val Ser
 60 65 70

acg gcg gag aaa gcg tcg gag att gta ctt caa ccc att aga gaa atc 353
 Thr Ala Glu Lys Ala Ser Glu Ile Val Leu Gln Pro Ile Arg Glu Ile
 75 80 85

tcc ggt ctt att aag ttg cct ggc tcc aag tct cta tca aat aga att c 402
 Ser Gly Leu Ile Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile
 90 95 100 105

<210> 13
 <211> 105
 <212> PRT
 <213> Arabidopsis thaliana

<400> 13

Met Ala Gln Val Ser Arg Ile Cys Asn Gly Val Gln Asn Pro Ser Leu
 1 5 10 15

Ile Ser Asn Leu Ser Lys Ser Ser Gln Arg Lys Ser Pro Leu Ser Val
 20 25 30

Ser Leu Lys Thr Gln Gln His Pro Arg Ala Tyr Pro Ile Ser Ser Ser
 35 40 45

Trp Gly Leu Lys Lys Ser Gly Met Thr Leu Ile Gly Ser Glu Leu Arg
 50 55 60

Pro Leu Lys Val Met Ser Ser Val Ser Thr Ala Glu Lys Ala Ser Glu
 65 70 75 80

Ile Val Leu Gln Pro Ile Arg Glu Ile Ser Gly Leu Ile Lys Leu Pro
 85 90 95

Gly Ser Lys Ser Leu Ser Asn Arg Ile
 100 105

<210> 14
 <211> 233
 <212> DNA
 <213> Petunia x hybrida

<220>

<221> CDS

<222> (14)..(232)

<400> 14

agatctttca aga atg gca caa att aac aac atg gct caa ggg ata caa 49
Met Ala Gln Ile Asn Asn Met Ala Gln Gly Ile Gln
1 5 10

acc ctt aat ccc aat tcc aat ttc cat aaa ccc caa gtt cct aaa tct 97
Thr Leu Asn Pro Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser
15 20 25

tca agt ttt ctt gtt ttt gga tct aaa aaa ctg aaa aat tca gca aat 145
Ser Ser Phe Leu Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn
30 35 40

tct atg ttg gtt ttg aaa aaa gat tca att ttt atg caa aag ttt tgt 193
Ser Met Leu Val Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys
45 50 55 60

tcc ttt agg att tca gca tca gtg gct aca gcc tgc atg c 233
Ser Phe Arg Ile Ser Ala Ser Val Ala Thr Ala Cys Met
65 70

<210> 15

<211> 73

<212> PRT

<213> Petunia x hybrida

<400> 15

Met Ala Gln Ile Asn Asn Met Ala Gln Gly Ile Gln Thr Leu Asn Pro
1 5 10 15

Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser Ser Ser Phe Leu
20 25 30

Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val
35 40 45

Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys Ser Phe Arg Ile
50 55 60

Ser Ala Ser Val Ala Thr Ala Cys Met
65 70

<210> 16

<211> 352

<212> DNA
<213> Petunia x hybrida

<220>
<221> CDS
<222> (49)..(351)

<400> 16
agatctgcta gaaataattt tgtttaactt taagaaggag atatatcc atg gca caa 57
Met Ala Gln
1

att aac aac atg gct caa ggg ata caa acc ctt aat ccc aat tcc aat 105
Ile Asn Asn Met Ala Gln Gly Ile Gln Thr Leu Asn Pro Asn Ser Asn
5 10 15

ttc cat aaa ccc caa gtt cct aaa tct tca agt ttt ctt gtt ttt gga 153
Phe His Lys Pro Gln Val Pro Lys Ser Ser Ser Phe Leu Val Phe Gly
20 25 30 35

tct aaa aaa ctg aaa aat tca gca aat tct atg ttg gtt ttg aaa aaa 201
Ser Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val Leu Lys Lys
40 45 50

gat tca att ttt atg caa aag ttt tgt tcc ttt agg att tca gca tca 249
Asp Ser Ile Phe Met Gln Lys Phe Cys Ser Phe Arg Ile Ser Ala Ser
55 60 65

gtg gct aca gca cag aag cct tct gag ata gtg ttg caa ccc att aaa 297
Val Ala Thr Ala Gln Lys Pro Ser Glu Ile Val Leu Gln Pro Ile Lys
70 75 80

gag att tca ggc act gtt aaa ttg cct ggc tct aaa tca tta tct aat 345
Glu Ile Ser Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn
85 90 95

aga att c 352
Arg Ile
100

<210> 17
<211> 101
<212> PRT
<213> Petunia x hybrida

<400> 17

Met Ala Gln Ile Asn Asn Met Ala Gln Gly Ile Gln Thr Leu Asn Pro
1 5 10 15

Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser Ser Ser Phe Leu
20 25 30

130

F

Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val
35 40 45

Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys Ser Phe Arg Ile
50 55 60

Ser Ala Ser Val Ala Thr Ala Gln Lys Pro Ser Glu Ile Val Leu Gln
65 70 75 80

Pro Ile Lys Glu Ile Ser Gly Thr Val Lys Leu Pro Gly Ser Lys Ser
85 90 95

Leu Ser Asn Arg Ile
100

<210> 18
<211> 28
<212> PRT
<213> Agrobacterium sp.

<220>
<221> UNSURE
<222> (1)..(18)
<223> Xaa = Unknown

<400> 18

Xaa His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser Ser Gly
1 5 10 15

Leu Xaa Gly Thr Val Arg Ile Pro Gly Asp Lys Met
20 25

<210> 19
<211> 13
<212> PRT
<213> Agrobacterium sp.

<400> 19

Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val
1 5 10

<210> 20
<211> 15
<212> PRT

<213> Agrobacterium sp.

<400> 20

Ile Thr Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys
1 5 10 15

<210> 21

<211> 17

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic

<400> 21

atgathgayg artaycc

17

<210> 22

<211> 17

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (1)..(17)

<223> R = A or G;

Y = C or T/U;

N = A or C or G or T/U;

H = A or C or T/U

<400> 22

gargaygtna thaacac

17

<210> 23

<211> 17

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (1)..(17)

<223> R = A or G;

Y = C or T/U;

N = A or C or G or T/U;

132

F

H = A or C or T/U

<400> 23
gargaygtna thaatac 17

<210> 24
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 24
cgtggataga tctaggaaga caaccatggc tcacggtc 38

<210> 25
<211> 44
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 25
ggatagatta aggaagacgc gcatgcttca cgggtgcaagc agcc 44

<210> 26
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 26
ggctgcctga tgagctccac aatcgccatc gatgg 35

<210> 27
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 27
cgtcgctcgt cgtgcgtggc cgccctgacg gc 32

<210> 28
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 28
cgggcaaggc catgcaggct atgggcgcc

29

<210> 29
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 29
cgggctgccg cctgactatg ggcctcgtcg g

31

<210> 30
<211> 15
<212> PRT
<213> Pseudomonas sp.

<220>
<221> NON_CONS
<222> (1)..(1)
<223> Xaa = unknown

<400> 30

Xaa	His	Ser	Ala	Ser	Pro	Lys	Pro	Ala	Thr	Ala	Arg	Arg	Ser	Glu
1				5					10				15	

<210> 31
<211> 17
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<220>
<221> misc_feature
<222> (1)..(17)
<223> B = C or G or T
S = G or C

27
134

F

Y = C or T

<400> 31
gcggtbgcsg gytts_g

17

<210> 32
<211> 16
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 32

Pro	Gly	Asp	Lys	Ser	Ile	Ser	His	Arg	Ser	Phe	Met	Phe	Gly	Gly	Leu
1				5				10					15		

<210> 33
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 33

Leu	Asp	Phe	Gly	Asn	Ala	Ala	Thr	Gly	Cys	Arg	Leu	Thr
1				5				10				

<210> 34
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 34
cggcaatgcc gccaccggcg cgcgcc

26

<210> 35
<211> 49
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 35

135

F

ggacggctgc ttgcaccgtag aagcatgctt aagcttggcg taatcatgg

49

<210> 36
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 36
ggaagacgcc cagaattcac ggtgcaagca gccgg

35

<210> 37
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<220>
<221> NON_CONS
<222> (2)..(2)
<223> Xaa = Gly, Ser, Thr, Cys, Tyr, Asn, Gln, Asp, or Glu

<220>
<221> NON_CONS
<222> (4)..(4)
<223> Xaa = Ser or Thr

<400> 37

Arg Xaa His Xaa Glu
1 5

<210> 38
<211> 4
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<220>
<221> NON_CONS
<222> (4)..(4)
<223> Xaa = Ser or Thr

<400> 38

Gly Asp Lys Xaa

1

<210> 39

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic

<220>

<221> NON_CONS

<222> (4)..(4)

<223> Xaa=Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys,
Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val

<400> 39

Ser Ala Gln Xaa Lys

1

5

<210> 40

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic

<220>

<221> NON_CONS

<222> (2)..(2)

<223> Xaa=Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys,
Met,

Phe, Pro, Ser, Thr, Trp, Tyr or Val

<400> 40

Asn Xaa Thr Arg

1

<210> 41

<211> 1287

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(1287)

137

A

<400> 41

atg aaa cga gat aag gtg cag acc tta cat gga gaa ata cat att ccc	48
Met Lys Arg Asp Lys Val Gln Thr Leu His Gly Glu Ile His Ile Pro	
1 5 10 15	
ggg gat aaa tcc att tct cac cgc tct gtt atg ttt ggc gcg cta gcg	96
Gly Asp Lys Ser Ile Ser His Arg Ser Val Met Phe Gly Ala Leu Ala	
20 25 30	
gca ggc aca aca aca gtt aaa aac ttt ctg ccg gga gca gat tgt ctg	144
Ala Gly Thr Thr Thr Val Lys Asn Phe Leu Pro Gly Ala Asp Cys Leu	
35 40 45	
agc acg atc gat tgc ttt aga aaa atg ggt gtt cac att gag caa agc	192
Ser Thr Ile Asp Cys Phe Arg Lys Met Gly Val His Ile Glu Gln Ser	
50 55 60	
agc agc gat gtc gtg att cac gga aaa gga atc gat gcc ctg aaa gag	240
Ser Ser Asp Val Val Ile His Gly Lys Gly Ile Asp Ala Leu Lys Glu	
65 70 75 80	
cca gaa agc ctt tta gat gtc gga aat tca ggt aca acg att cgc ctg	288
Pro Glu Ser Leu Leu Asp Val Gly Asn Ser Gly Thr Thr Ile Arg Leu	
85 90 95	
atg ctc gga ata ttg gcg ggc cgt cct ttt tac agc gcg gta gcc gga	336
Met Leu Gly Ile Leu Ala Gly Arg Pro Phe Tyr Ser Ala Val Ala Gly	
100 105 110	
gat gag agc att gcg aaa cgc cca atg aag cgt gtg act gag cct ttg	384
Asp Glu Ser Ile Ala Lys Arg Pro Met Lys Arg Val Thr Glu Pro Leu	
115 120 125	
aaa aaa atg ggg gct aaa atc gac ggc aga gcc ggc gga gag ttt aca	432
Lys Lys Met Gly Ala Lys Ile Asp Gly Arg Ala Gly Gly Glu Phe Thr	
130 135 140	
ccg ctg tca gtg agc ggc gct tca tta aaa gga att gat tat gta tca	480
Pro Leu Ser Val Ser Gly Ala Ser Leu Lys Gly Ile Asp Tyr Val Ser	
145 150 155 160	
cct gtt gca agc gcg caa att aaa tct gct gtt ttg ctg gcc gga tta	528
Pro Val Ala Ser Ala Gln Ile Lys Ser Ala Val Leu Leu Ala Gly Leu	
165 170 175	
cag gct gag ggc aca aca act gta aca gag ccc cat aaa tct cgg gac	576
Gln Ala Glu Gly Thr Thr Thr Val Thr Glu Pro His Lys Ser Arg Asp	
180 185 190	
cac act gag cgg atg ctt tct gct ttt ggc gtt aag ctt tct gaa gat	624
His Thr Glu Arg Met Leu Ser Ala Phe Gly Val Lys Leu Ser Glu Asp	
195 200 205	

caa acg agt gtt tcc att gct ggt ggc cag aaa ctg aca gct gct gat	672
Gln Thr Ser Val Ser Ile Ala Gly Gly Gln Lys Leu Thr Ala Ala Asp	
210 215 220	
att ttt gtt cct gga gac att tct tca gcc gcg ttt ttc ctt gct gct	720
Ile Phe Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Phe Leu Ala Ala	
225 230 235 240	
ggc gcg atg gtt cca aac agc aga att gta ttg aaa aac gta ggt tta	768
Gly Ala Met Val Pro Asn Ser Arg Ile Val Leu Lys Asn Val Gly Leu	
245 250 255	
aat ccg act cgg aca ggt att att gat gtc ctt caa aac atg ggg gca	816
Asn Pro Thr Arg Thr Gly Ile Ile Asp Val Leu Gln Asn Met Gly Ala	
260 265 270	
aaa ctt gaa atc aaa cca tct gct gat agc ggt gca gag cct tat gga	864
Lys Leu Glu Ile Lys Pro Ser Ala Asp Ser Gly Ala Glu Pro Tyr Gly	
275 280 285	
gat ttg att ata gaa acg tca tct cta aag gca gtt gaa atc gga gga	912
Asp Leu Ile Ile Glu Thr Ser Ser Leu Lys Ala Val Glu Ile Gly Gly	
290 295 300	
gat atc att ccg cgt tta att gat gag atc cct atc atc gcg ctt ctt	960
Asp Ile Ile Pro Arg Leu Ile Asp Glu Ile Pro Ile Ile Ala Leu Leu	
305 310 315 320	
gcg act cag gcg gaa gga acc acc gtt att aag gac gcg gca gag cta	1008
Ala Thr Gln Ala Glu Gly Thr Thr Val Ile Lys Asp Ala Ala Glu Leu	
325 330 335	
aaa gtg aaa gaa aca aac cgt att gat act gtt gtt tct gag ctt cgc	1056
Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Val Val Ser Glu Leu Arg	
340 345 350	
aag ctg ggt gct gaa att gaa ccg aca gca gat gga atg aag gtt tat	1104
Lys Leu Gly Ala Glu Ile Glu Pro Thr Ala Asp Gly Met Lys Val Tyr	
355 360 365	
ggc aaa caa acg ttg aaa ggc ggc gct gca gtg tcc agc cac gga gat	1152
Gly Lys Gln Thr Leu Lys Gly Gly Ala Ala Val Ser Ser His Gly Asp	
370 375 380	
cat cga atc gga atg atg ctt ggt att gct tcc tgt ata acg gag gag	1200
His Arg Ile Gly Met Met Leu Gly Ile Ala Ser Cys Ile Thr Glu Glu	
385 390 395 400	
ccg att gaa atc gag cac acg gat gcc att cac gtt tct tat cca acc	1248
Pro Ile Glu Ile Glu His Thr Asp Ala Ile His Val Ser Tyr Pro Thr	
405 410 415	
ttc ttc gag cat tta aat aag ctt tcg aaa aaa tcc tga	1287
Phe Phe Glu His Leu Asn Lys Leu Ser Lys Lys Ser	

420

425

<210> 42
 <211> 428
 <212> PRT
 <213> Bacillus subtilis

<400> 42

Met Lys Arg Asp Lys Val Gln Thr Leu His Gly Glu Ile His Ile Pro
 1 5 10 15

Gly Asp Lys Ser Ile Ser His Arg Ser Val Met Phe Gly Ala Leu Ala
 20 25 30

Ala Gly Thr Thr Thr Val Lys Asn Phe Leu Pro Gly Ala Asp Cys Leu
 35 40 45

Ser Thr Ile Asp Cys Phe Arg Lys Met Gly Val His Ile Glu Gln Ser
 50 55 60

Ser Ser Asp Val Val Ile His Gly Lys Gly Ile Asp Ala Leu Lys Glu
 65 70 75 80

Pro Glu Ser Leu Leu Asp Val Gly Asn Ser Gly Thr Thr Ile Arg Leu
 85 90 95

Met Leu Gly Ile Leu Ala Gly Arg Pro Phe Tyr Ser Ala Val Ala Gly
 100 105 110

Asp Glu Ser Ile Ala Lys Arg Pro Met Lys Arg Val Thr Glu Pro Leu
 115 120 125

Lys Lys Met Gly Ala Lys Ile Asp Gly Arg Ala Gly Gly Glu Phe Thr
 130 135 140

Pro Leu Ser Val Ser Gly Ala Ser Leu Lys Gly Ile Asp Tyr Val Ser
 145 150 155 160

Pro Val Ala Ser Ala Gln Ile Lys Ser Ala Val Leu Leu Ala Gly Leu
 165 170 175

Gln	Ala	Glu	Gly	Thr	Thr	Thr	Val	Thr	Glu	Pro	His	Lys	Ser	Arg	Asp
			180					185					190		
His	Thr	Glu	Arg	Met	Leu	Ser	Ala	Phe	Gly	Val	Lys	Leu	Ser	Glu	Asp
		195					200					205			
Gln	Thr	Ser	Val	Ser	Ile	Ala	Gly	Gly	Gln	Lys	Leu	Thr	Ala	Ala	Asp
	210					215					220				
Ile	Phe	Val	Pro	Gly	Asp	Ile	Ser	Ser	Ala	Ala	Phe	Phe	Leu	Ala	Ala
225					230					235					240
Gly	Ala	Met	Val	Pro	Asn	Ser	Arg	Ile	Val	Leu	Lys	Asn	Val	Gly	Leu
				245					250					255	
Asn	Pro	Thr	Arg	Thr	Gly	Ile	Ile	Asp	Val	Leu	Gln	Asn	Met	Gly	Ala
			260					265					270		
Lys	Leu	Glu	Ile	Lys	Pro	Ser	Ala	Asp	Ser	Gly	Ala	Glu	Pro	Tyr	Gly
		275					280					285			
Asp	Leu	Ile	Ile	Glu	Thr	Ser	Ser	Leu	Lys	Ala	Val	Glu	Ile	Gly	Gly
	290					295					300				
Asp	Ile	Ile	Pro	Arg	Leu	Ile	Asp	Glu	Ile	Pro	Ile	Ile	Ala	Leu	Leu
305					310					315					320
Ala	Thr	Gln	Ala	Glu	Gly	Thr	Thr	Val	Ile	Lys	Asp	Ala	Ala	Glu	Leu
				325					330					335	
Lys	Val	Lys	Glu	Thr	Asn	Arg	Ile	Asp	Thr	Val	Val	Ser	Glu	Leu	Arg
			340					345					350		
Lys	Leu	Gly	Ala	Glu	Ile	Glu	Pro	Thr	Ala	Asp	Gly	Met	Lys	Val	Tyr
		355					360					365			
Gly	Lys	Gln	Thr	Leu	Lys	Gly	Gly	Ala	Ala	Val	Ser	Ser	His	Gly	Asp
	370					375					380				
His	Arg	Ile	Gly	Met	Met	Leu	Gly	Ile	Ala	Ser	Cys	Ile	Thr	Glu	Glu
385					390					395					400

141

F

Pro Ile Glu Ile Glu His Thr Asp Ala Ile His Val Ser Tyr Pro Thr
 405 410 415

Phe Phe Glu His Leu Asn Lys Leu Ser Lys Lys Ser
 420 425

<210> 43
 <211> 1293
 <212> DNA
 <213> Staphylococcus aureus

<220>
 <221> CDS
 <222> (1)..(1293)

<400> 43
 atg gta aat gaa caa atc att gat att tca ggt ccg tta aag ggc gaa 48
 Met Val Asn Glu Gln Ile Ile Asp Ile Ser Gly Pro Leu Lys Gly Glu
 1 5 10 15
 ata gaa gtg ccg ggc gat aag tca atg aca cac cgt gca atc atg ttg 96
 Ile Glu Val Pro Gly Asp Lys Ser Met Thr His Arg Ala Ile Met Leu
 20 25 30
 gcg tcg cta gct gaa ggt gta tct act ata tat aag cca cta ctt ggc 144
 Ala Ser Leu Ala Glu Gly Val Ser Thr Ile Tyr Lys Pro Leu Leu Gly
 35 40 45
 gaa gat tgt cgt cgt acg atg gac att ttc cga cac tta ggt gta gaa 192
 Glu Asp Cys Arg Arg Thr Met Asp Ile Phe Arg His Leu Gly Val Glu
 50 55 60
 atc aaa gaa gat gat gaa aaa tta gtt gtg act tcc cca gga tat caa 240
 Ile Lys Glu Asp Asp Glu Lys Leu Val Val Thr Ser Pro Gly Tyr Gln
 65 70 75 80
 gtt aac acg cca cat caa gta ttg tat aca ggt aat tct ggt acg aca 288
 Val Asn Thr Pro His Gln Val Leu Tyr Thr Gly Asn Ser Gly Thr Thr
 85 90 95
 aca cga tta ttg gca ggt ttg tta agt ggt tta ggt aat gaa agt gtt 336
 Thr Arg Leu Leu Ala Gly Leu Leu Ser Gly Leu Gly Asn Glu Ser Val
 100 105 110
 ttg tct ggc gat gtt tca att ggt aaa agg cca atg gat cgt gtc ttg 384
 Leu Ser Gly Asp Val Ser Ile Gly Lys Arg Pro Met Asp Arg Val Leu
 115 120 125
 aga cca ttg aaa ctt atg gat gcg aat att gaa ggt att gaa gat aat 432
 Arg Pro Leu Lys Leu Met Asp Ala Asn Ile Glu Gly Ile Glu Asp Asn

142

F

130	135	140	
tat aca cca tta att att aag cca tct gtc ata aaa ggt ata aat tat			480
Tyr Thr Pro Leu Ile Ile Lys Pro Ser Val Ile Lys Gly Ile Asn Tyr			
145	150	155	160
caa atg gaa gtt gca agt gca caa gta aaa agt gcc att tta ttt gca			528
Gln Met Glu Val Ala Ser Ala Gln Val Lys Ser Ala Ile Leu Phe Ala			
	165	170	175
agt ttg ttt tct aag gaa ccg acc atc att aaa gaa tta gat gta agt			576
Ser Leu Phe Ser Lys Glu Pro Thr Ile Ile Lys Glu Leu Asp Val Ser			
	180	185	190
cga aat cat act gag acg atg ttc aaa cat ttt aat att cca att gaa			624
Arg Asn His Thr Glu Thr Met Phe Lys His Phe Asn Ile Pro Ile Glu			
	195	200	205
gca gaa ggg tta tca att aat aca acc cct gaa gca att cga tac att			672
Ala Glu Gly Leu Ser Ile Asn Thr Thr Pro Glu Ala Ile Arg Tyr Ile			
	210	215	220
aaa cct gca gat ttt cat gtt cct ggc gat att tca tct gca gcg ttc			720
Lys Pro Ala Asp Phe His Val Pro Gly Asp Ile Ser Ser Ala Ala Phe			
	225	230	235
ttt att gtt gca gca ctt atc aca cca gga agt gat gta aca att cat			768
Phe Ile Val Ala Ala Leu Ile Thr Pro Gly Ser Asp Val Thr Ile His			
	245	250	255
aat gtt gga atc aat caa aca cgt tca ggt att att gat att gtt gaa			816
Asn Val Gly Ile Asn Gln Thr Arg Ser Gly Ile Ile Asp Ile Val Glu			
	260	265	270
aaa atg ggc ggt aat atc caa ctt ttc aat caa aca act ggt gct gaa			864
Lys Met Gly Gly Asn Ile Gln Leu Phe Asn Gln Thr Thr Gly Ala Glu			
	275	280	285
cct act gct tct att cgt att caa tac aca cca atg ctt caa cca ata			912
Pro Thr Ala Ser Ile Arg Ile Gln Tyr Thr Pro Met Leu Gln Pro Ile			
	290	295	300
aca atc gaa gga gaa tta gtt cca aaa gca att gat gaa ctg cct gta			960
Thr Ile Glu Gly Glu Leu Val Pro Lys Ala Ile Asp Glu Leu Pro Val			
	305	310	315
ata gca tta ctt tgt aca caa gca gtt ggc acg agt aca att aaa gat			1008
Ile Ala Leu Leu Cys Thr Gln Ala Val Gly Thr Ser Thr Ile Lys Asp			
	325	330	335
gcc gag gaa tta aaa gta aaa gaa aca aat aga att gat aca acg gct			1056
Ala Glu Glu Leu Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Thr Ala			
	340	345	350

gat atg tta aac ttg tta ggg ttt gaa tta caa cca act aat gat gga 1104
 Asp Met Leu Asn Leu Leu Gly Phe Glu Leu Gln Pro Thr Asn Asp Gly
 355 360 365

ttg att att cat ccg tca gaa ttt aaa aca aat gca aca gat att tta 1152
 Leu Ile Ile His Pro Ser Glu Phe Lys Thr Asn Ala Thr Asp Ile Leu
 370 375 380

act gat cat cga ata gga atg atg ctt gca gtt gct tgt gta ctt tca 1200
 Thr Asp His Arg Ile Gly Met Met Leu Ala Val Ala Cys Val Leu Ser
 385 390 395 400

agc gag cct gtc aaa atc aaa caa ttt gat gct gta aat gta tca ttt 1248
 Ser Glu Pro Val Lys Ile Lys Gln Phe Asp Ala Val Asn Val Ser Phe
 405 410 415

cca gga ttt tta cca aaa cta aag ctt tta caa aat gag gga taa 1293
 Pro Gly Phe Leu Pro Lys Leu Lys Leu Leu Gln Asn Glu Gly
 420 425 430

<210> 44
 <211> 430
 <212> PRT
 <213> Staphylococcus aureus

<400> 44

Met Val Asn Glu Gln Ile Ile Asp Ile Ser Gly Pro Leu Lys Gly Glu
 1 5 10 15

Ile Glu Val Pro Gly Asp Lys Ser Met Thr His Arg Ala Ile Met Leu
 20 25 30

Ala Ser Leu Ala Glu Gly Val Ser Thr Ile Tyr Lys Pro Leu Leu Gly
 35 40 45

Glu Asp Cys Arg Arg Thr Met Asp Ile Phe Arg His Leu Gly Val Glu
 50 55 60

Ile Lys Glu Asp Asp Glu Lys Leu Val Val Thr Ser Pro Gly Tyr Gln
 65 70 75 80

Val Asn Thr Pro His Gln Val Leu Tyr Thr Gly Asn Ser Gly Thr Thr
 85 90 95

Thr Arg Leu Leu Ala Gly Leu Leu Ser Gly Leu Gly Asn Glu Ser Val
 100 105 110

144

7

Leu	Ser	Gly	Asp	Val	Ser	Ile	Gly	Lys	Arg	Pro	Met	Asp	Arg	Val	Leu
		115					120					125			
Arg	Pro	Leu	Lys	Leu	Met	Asp	Ala	Asn	Ile	Glu	Gly	Ile	Glu	Asp	Asn
	130					135					140				
Tyr	Thr	Pro	Leu	Ile	Ile	Lys	Pro	Ser	Val	Ile	Lys	Gly	Ile	Asn	Tyr
145					150					155					160
Gln	Met	Glu	Val	Ala	Ser	Ala	Gln	Val	Lys	Ser	Ala	Ile	Leu	Phe	Ala
				165					170					175	
Ser	Leu	Phe	Ser	Lys	Glu	Pro	Thr	Ile	Ile	Lys	Glu	Leu	Asp	Val	Ser
			180					185					190		
Arg	Asn	His	Thr	Glu	Thr	Met	Phe	Lys	His	Phe	Asn	Ile	Pro	Ile	Glu
		195					200					205			
Ala	Glu	Gly	Leu	Ser	Ile	Asn	Thr	Thr	Pro	Glu	Ala	Ile	Arg	Tyr	Ile
	210					215					220				
Lys	Pro	Ala	Asp	Phe	His	Val	Pro	Gly	Asp	Ile	Ser	Ser	Ala	Ala	Phe
225					230					235					240
Phe	Ile	Val	Ala	Ala	Leu	Ile	Thr	Pro	Gly	Ser	Asp	Val	Thr	Ile	His
				245					250					255	
Asn	Val	Gly	Ile	Asn	Gln	Thr	Arg	Ser	Gly	Ile	Ile	Asp	Ile	Val	Glu
			260					265					270		
Lys	Met	Gly	Gly	Asn	Ile	Gln	Leu	Phe	Asn	Gln	Thr	Thr	Gly	Ala	Glu
		275					280					285			
Pro	Thr	Ala	Ser	Ile	Arg	Ile	Gln	Tyr	Thr	Pro	Met	Leu	Gln	Pro	Ile
		290				295					300				
Thr	Ile	Glu	Gly	Glu	Leu	Val	Pro	Lys	Ala	Ile	Asp	Glu	Leu	Pro	Val
305					310					315					320

Ile Ala Leu Leu Cys Thr Gln Ala Val Gly Thr Ser Thr Ile Lys Asp
325 330 335

Ala Glu Glu Leu Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Thr Ala
340 345 350

Asp Met Leu Asn Leu Leu Gly Phe Glu Leu Gln Pro Thr Asn Asp Gly
355 360 365

Leu Ile Ile His Pro Ser Glu Phe Lys Thr Asn Ala Thr Asp Ile Leu
370 375 380

Thr Asp His Arg Ile Gly Met Met Leu Ala Val Ala Cys Val Leu Ser
385 390 395 400

Ser Glu Pro Val Lys Ile Lys Gln Phe Asp Ala Val Asn Val Ser Phe
405 410 415

Pro Gly Phe Leu Pro Lys Leu Lys Leu Leu Gln Asn Glu Gly
420 425 430

<210> 45
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 45
ggaacatatg aaacgagata aggtgcag

28

<210> 46
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 46
ggaattcaaa cttcaggatc ttgagataga aaatg

35

<210> 47
<211> 28

1410

7

<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 47
ggggccatgg taaatgaaca aatcattg

28

<210> 48
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 48
gggggagctc attatccctc attttgtaaa agc

33

<210> 49
<211> 480
<212> PRT
<213> Saccharomyces cerevisiae

<400> 49

Leu Thr Asp Glu Thr Leu Val Tyr Pro Phe Lys Asp Ile Pro Ala Asp
1 5 10 15

Gln Gln Lys Val Val Ile Pro Pro Gly Ser Lys Ser Ile Ser Asn Arg
20 25 30

Ala Leu Ile Leu Ala Ala Leu Gly Glu Gly Gln Cys Lys Ile Lys Asn
35 40 45

Leu Leu His Ser Asp Asp Thr Lys His Met Leu Thr Ala Val His Glu
50 55 60

Leu Lys Gly Ala Thr Ile Ser Trp Glu Asp Asn Gly Glu Thr Val Val
65 70 75 80

Val Glu Gly His Gly Gly Ser Thr Leu Ser Ala Cys Ala Asp Pro Leu
85 90 95

Tyr Leu Gly Asn Ala Gly Thr Ala Ser Arg Phe Leu Thr Ser Leu Ala
100 105 110

Ala Leu Val Asn Ser Thr Ser Ser Gln Lys Tyr Ile Val Leu Thr Gly
115 120 125

Asn Ala Arg Met Gln Gln Arg Pro Ile Ala Pro Leu Val Asp Ser Leu

130		135		140
Arg Ala Asn Gly Thr Lys Ile Glu Tyr Leu Asn Asn Glu Gly Ser Leu				
145		150		155 160
Pro Ile Lys Val Tyr Thr Asp Ser Val Phe Lys Gly Gly Arg Ile Glu				
	165		170	175
Leu Ala Ala Thr Val Ser Ser Gln Tyr Val Ser Ser Ile Leu Met Cys				
	180		185	190
Ala Pro Tyr Ala Glu Glu Pro Val Thr Leu Ala Leu Val Gly Gly Lys				
	195		200	205
Pro Ile Ser Lys Leu Tyr Val Asp Met Thr Ile Lys Met Met Glu Lys				
	210		215	220
Phe Gly Ile Asn Val Glu Thr Ser Thr Thr Glu Pro Tyr Thr Tyr Tyr				
225		230		235 240
Ile Pro Lys Gly His Tyr Ile Asn Pro Ser Glu Tyr Val Ile Glu Ser				
	245		250	255
Asp Ala Ser Ser Ala Thr Tyr Pro Leu Ala Phe Ala Ala Met Thr Gly				
	260		265	270
Thr Thr Val Thr Val Pro Asn Ile Gly Phe Glu Ser Leu Gln Gly Asp				
	275		280	285
Ala Arg Phe Ala Arg Asp Val Leu Lys Pro Met Gly Cys Lys Ile Thr				
	290		295	300
Gln Thr Ala Thr Ser Thr Thr Val Ser Gly Pro Pro Val Gly Thr Leu				
305		310		315 320
Lys Pro Leu Lys His Val Asp Met Glu Pro Met Thr Asp Ala Phe Leu				
	325		330	335
Thr Ala Cys Val Val Ala Ala Ile Ser His Asp Ser Asp Pro Asn Ser				
	340		345	350
Ala Asn Thr Thr Thr Ile Glu Gly Ile Ala Asn Gln Arg Val Lys Glu				
	355		360	365
Cys Asn Arg Ile Leu Ala Met Ala Thr Glu Leu Ala Lys Phe Gly Val				
	370		375	380
Lys Thr Thr Glu Leu Pro Asp Gly Ile Gln Val His Gly Leu Asn Ser				
385		390		395 400
Ile Lys Asp Leu Lys Val Pro Ser Asp Ser Ser Gly Pro Val Gly Val				
	405		410	415
Cys Thr Tyr Asp Asp His Arg Val Ala Met Ser Phe Ser Leu Leu Ala				

148

F

420

425

430

Gly Met Val Asn Ser Gln Asn Glu Arg Asp Glu Val Ala Asn Pro Val
 435 440 445

Arg Ile Leu Glu Arg His Cys Thr Gly Lys Thr Trp Pro Gly Trp Trp
 450 455 460

Asp Val Leu His Ser Glu Leu Gly Ala Lys Leu Asp Gly Ala Glu Pro
 465 470 475 480

<210> 50

<211> 460

<212> PRT

<213> *Aspergillus nidulans*

<400> 50

Leu Ala Pro Ser Ile Glu Val His Pro Gly Val Ala His Ser Ser Asn
 1 5 10 15

Val Ile Cys Ala Pro Pro Gly Ser Lys Ser Ile Ser Asn Arg Ala Leu
 20 25 30

Val Leu Ala Ala Leu Gly Ser Gly Thr Cys Arg Ile Lys Asn Leu Leu
 35 40 45

His Ser Asp Asp Thr Glu Val Met Leu Asn Ala Leu Glu Arg Leu Gly
 50 55 60

Ala Ala Thr Phe Ser Trp Glu Glu Glu Gly Glu Val Leu Val Val Asn
 65 70 75 80

Gly Lys Gly Gly Asn Leu Gln Ala Ser Ser Ser Pro Leu Tyr Leu Gly
 85 90 95

Asn Ala Gly Thr Ala Ser Arg Phe Leu Thr Thr Val Ala Thr Leu Ala
 100 105 110

Asn Ser Ser Thr Val Asp Ser Ser Val Leu Thr Gly Asn Asn Arg Met
 115 120 125

Lys Gln Arg Pro Ile Gly Asp Leu Val Asp Ala Leu Thr Ala Asn Val
 130 135 140

Leu Pro Leu Asn Thr Ser Lys Gly Arg Ala Ser Leu Pro Leu Lys Ile
 145 150 155 160

Ala Ala Ser Gly Gly Phe Ala Gly Gly Asn Ile Asn Leu Ala Ala Lys
 165 170 175

Val Ser Ser Gln Tyr Val Ser Ser Leu Leu Met Cys Ala Pro Tyr Ala
 180 185 190

Lys	Glu	Pro	Val	Thr	Leu	Arg	Leu	Val	Gly	Gly	Lys	Pro	Ile	Ser	Gln
	195						200					205			
Pro	Tyr	Ile	Asp	Met	Thr	Thr	Ala	Met	Met	Arg	Ser	Phe	Gly	Ile	Asp
	210						215				220				
Val	Gln	Lys	Ser	Thr	Thr	Glu	Glu	His	Thr	Tyr	His	Ile	Pro	Gln	Gly
	225					230				235					240
Arg	Tyr	Val	Asn	Pro	Ala	Glu	Tyr	Val	Ile	Glu	Ser	Asp	Ala	Ser	Cys
			245						250					255	
Ala	Thr	Tyr	Pro	Leu	Ala	Val	Ala	Ala	Val	Thr	Gly	Thr	Thr	Cys	Thr
			260					265					270		
Val	Pro	Asn	Ile	Gly	Ser	Ala	Ser	Leu	Gln	Gly	Asp	Ala	Arg	Phe	Ala
	275						280					285			
Val	Glu	Val	Leu	Arg	Pro	Met	Gly	Cys	Thr	Val	Glu	Gln	Thr	Glu	Thr
	290					295					300				
Ser	Thr	Thr	Val	Thr	Gly	Pro	Ser	Asp	Gly	Ile	Leu	Arg	Ala	Thr	Ser
	305				310					315					320
Lys	Arg	Gly	Tyr	Gly	Thr	Asn	Asp	Arg	Cys	Val	Pro	Arg	Cys	Phe	Arg
				325					330					335	
Thr	Gly	Ser	His	Arg	Pro	Met	Glu	Lys	Ser	Gln	Thr	Thr	Pro	Pro	Val
			340					345					350		
Ser	Ser	Gly	Ile	Ala	Asn	Gln	Arg	Val	Lys	Glu	Cys	Asn	Arg	Ile	Lys
		355					360					365			
Ala	Met	Lys	Asp	Glu	Leu	Ala	Lys	Phe	Gly	Val	Ile	Cys	Arg	Glu	His
	370					375					380				
Asp	Asp	Gly	Leu	Glu	Ile	Asp	Gly	Ile	Asp	Arg	Ser	Asn	Leu	Arg	Gln
	385				390					395					400
Pro	Val	Gly	Gly	Val	Phe	Cys	Tyr	Asp	Asp	His	Arg	Val	Ala	Phe	Ser
				405					410					415	
Phe	Ser	Val	Leu	Ser	Leu	Val	Thr	Pro	Gln	Pro	Thr	Leu	Ile	Leu	Glu
			420					425					430		
Lys	Glu	Cys	Val	Gly	Lys	Thr	Trp	Pro	Gly	Trp	Trp	Asp	Thr	Leu	Arg
		435					440					445			
Gln	Leu	Phe	Lys	Val	Lys	Leu	Glu	Gly	Lys	Glu	Leu				
	450					455					460				

<210> 51
 <211> 444
 <212> PRT

150

7

<213> Brassica napus

<400> 51

Lys Ala Ser Glu Ile Val Leu Gln Pro Ile Arg Glu Ile Ser Gly Leu
1 5 10 15
Ile Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu
20 25 30
Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn Ser
35 40 45
Asp Asp Ile Asn Tyr Met Leu Asp Ala Leu Lys Lys Leu Gly Leu Asn
50 55 60
Val Glu Arg Asp Ser Val Asn Asn Arg Ala Val Val Glu Gly Cys Gly
65 70 75 80
Gly Ile Phe Pro Ala Ser Leu Asp Ser Lys Ser Asp Ile Glu Leu Tyr
85 90 95
Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
100 105 110
Ala Ala Gly Gly Asn Ala Ser Tyr Val Leu Asp Gly Val Pro Arg Met
115 120 125
Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
130 135 140
Ala Asp Val Glu Cys Thr Leu Gly Thr Asn Cys Pro Pro Val Arg Val
145 150 155 160
Asn Ala Asn Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
165 170 175
Ile Ser Ser Gln Tyr Leu Thr Ala Leu Leu Met Ala Ala Pro Leu Ala
180 185 190
Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Val Pro
195 200 205
Tyr Val Glu Met Thr Leu Lys Leu Met Glu Arg Phe Gly Val Ser Ala
210 215 220
Glu His Ser Asp Ser Trp Asp Arg Phe Phe Val Lys Gly Gly Gln Lys
225 230 235 240
Tyr Lys Ser Pro Gly Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
245 250 255
Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Glu Thr Val Thr Val
260 265 270

Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
275 280 285

Val Leu Glu Lys Met Gly Cys Lys Val Ser Trp Thr Glu Asn Ser Val
290 295 300

Thr Val Thr Gly Pro Ser Arg Asp Ala Phe Gly Met Arg His Leu Arg
305 310 315 320

Ala Val Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
325 330 335

Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Thr Ile Arg Asp Val
340 345 350

Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Ile Ala Ile Cys Thr
355 360 365

Glu Leu Arg Lys Leu Gly Ala Thr Val Glu Glu Gly Ser Asp Tyr Cys
370 375 380

Val Ile Thr Pro Pro Ala Lys Val Lys Pro Ala Glu Ile Asp Thr Tyr
385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp
405 410 415

Val Pro Val Thr Ile Lys Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
420 425 430

Asp Tyr Phe Gln Val Leu Glu Ser Ile Thr Lys His
435 440

<210> 52

<211> 444

<212> PRT

<213> Arabidopsis thaliana

<400> 52

Lys Ala Ser Glu Ile Val Leu Gln Pro Ile Arg Glu Ile Ser Gly Leu
1 5 10 15

Ile Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu
20 25 30

Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn Ser
35 40 45

Asp Asp Ile Asn Tyr Met Leu Asp Ala Leu Lys Arg Leu Gly Leu Asn
50 55 60

Val Glu Thr Asp Ser Glu Asn Asn Arg Ala Val Val Glu Gly Cys Gly

152

F

65		70		75		80
Gly Ile Phe Pro Ala Ser Ile Asp Ser Lys Ser Asp Ile Glu Leu Tyr						
	85			90		95
Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr						
	100			105		110
Ala Ala Gly Gly Asn Ala Ser Tyr Val Leu Asp Gly Val Pro Arg Met						
	115			120		125
Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly						
	130			135		140
Ala Asp Val Glu Cys Thr Leu Gly Thr Asn Cys Pro Pro Val Arg Val						
	145			150		155
Asn Ala Asn Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser						
				165		170
Ile Ser Ser Gln Tyr Leu Thr Ala Leu Leu Met Ser Ala Pro Leu Ala						
				180		185
Leu Gly Asp Val Glu Ile Glu Ile Val Asp Lys Leu Ile Ser Val Pro						
				195		200
Tyr Val Glu Met Thr Leu Lys Leu Met Glu Arg Phe Gly Val Ser Val						
				210		215
Glu His Ser Asp Ser Trp Asp Arg Phe Phe Val Lys Gly Gly Gln Lys						
				225		230
Tyr Lys Ser Pro Gly Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala						
				245		250
Cys Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Glu Thr Val Thr Val						
				260		265
Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu						
				275		280
Val Leu Glu Lys Met Gly Cys Lys Val Ser Trp Thr Glu Asn Ser Val						
				290		295
Thr Val Thr Gly Pro Pro Arg Asp Ala Phe Gly Met Arg His Leu Arg						
				305		310
Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu						
				325		330
Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Thr Ile Arg Asp Val						
				340		345
Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Ile Ala Ile Cys Thr						

153

F

355

360

365

Glu Leu Arg Lys Leu Gly Ala Thr Val Glu Glu Gly Ser Asp Tyr Cys
 370 375 380

Val Ile Thr Pro Pro Lys Lys Val Lys Thr Ala Glu Ile Asp Thr Tyr
 385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp
 405 410 415

Val Pro Ile Thr Ile Asn Asp Ser Gly Cys Thr Arg Lys Thr Phe Pro
 420 425 430

Asp Tyr Phe Gln Val Leu Glu Arg Ile Thr Lys His
 435 440

<210> 53
 <211> 444
 <212> PRT
 <213> Nicotiana tabacum

<400> 53

Lys Pro Asn Glu Ile Val Leu Gln Pro Ile Lys Asp Ile Ser Gly Thr
 1 5 10 15

Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu
 20 25 30

Ala Ala Leu Ser Lys Gly Arg Thr Val Val Asp Asn Leu Leu Ser Ser
 35 40 45

Asp Asp Ile His Tyr Met Leu Gly Ala Leu Lys Thr Leu Gly Leu His
 50 55 60

Val Glu Asp Asp Asn Glu Asn Gln Arg Ala Ile Val Glu Gly Cys Gly
 65 70 75 80

Gly Gln Phe Pro Val Gly Lys Lys Ser Glu Glu Glu Ile Gln Leu Phe
 85 90 95

Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
 100 105 110

Val Ala Gly Gly His Ser Arg Tyr Val Leu Asp Gly Val Pro Arg Met
 115 120 125

Arg Glu Arg Pro Ile Gly Asp Leu Val Asp Gly Leu Lys Gln Leu Gly
 130 135 140

Ala Glu Val Asp Cys Phe Leu Gly Thr Asn Cys Pro Pro Val Arg Ile
 145 150 155 160

Val	Ser	Lys	Gly	Gly	Leu	Pro	Gly	Gly	Lys	Val	Lys	Leu	Ser	Gly	Ser	165	170	175	
Ile	Ser	Ser	Gln	Tyr	Leu	Thr	Ala	Leu	Leu	Met	Ala	Ala	Pro	Leu	Ala	180	185	190	
Leu	Gly	Asp	Val	Glu	Ile	Glu	Ile	Ile	Asp	Lys	Leu	Ile	Ser	Val	Pro	195	200	205	
Tyr	Val	Glu	Met	Thr	Leu	Lys	Leu	Met	Glu	Arg	Phe	Gly	Val	Ser	Val	210	215	220	
Glu	His	Thr	Ser	Ser	Trp	Asp	Lys	Phe	Leu	Val	Arg	Gly	Gly	Gln	Lys	225	230	235	240
Tyr	Lys	Ser	Pro	Gly	Lys	Ala	Tyr	Val	Glu	Gly	Asp	Ala	Ser	Ser	Ala	245	250	255	
Ser	Tyr	Phe	Leu	Ala	Gly	Ala	Ala	Val	Thr	Gly	Gly	Thr	Val	Thr	Val	260	265	270	
Glu	Gly	Cys	Gly	Thr	Ser	Ser	Leu	Gln	Gly	Asp	Val	Lys	Phe	Ala	Glu	275	280	285	
Val	Leu	Glu	Lys	Met	Gly	Ala	Glu	Val	Thr	Trp	Thr	Glu	Asn	Ser	Val	290	295	300	
Thr	Val	Lys	Gly	Pro	Pro	Arg	Asn	Ser	Ser	Gly	Met	Lys	His	Leu	Arg	305	310	315	320
Ala	Val	Asp	Val	Asn	Met	Asn	Lys	Met	Pro	Asp	Val	Ala	Met	Thr	Leu	325	330	335	
Ala	Val	Val	Ala	Leu	Phe	Ala	Asp	Gly	Pro	Thr	Ala	Ile	Arg	Asp	Val	340	345	350	
Ala	Ser	Trp	Arg	Val	Lys	Glu	Thr	Glu	Arg	Met	Ile	Ala	Ile	Cys	Thr	355	360	365	
Glu	Leu	Arg	Lys	Leu	Gly	Ala	Thr	Val	Val	Glu	Gly	Ser	Asp	Tyr	Cys	370	375	380	
Ile	Ile	Thr	Pro	Pro	Glu	Lys	Leu	Asn	Val	Thr	Glu	Ile	Asp	Thr	Tyr	385	390	395	400
Asp	Asp	His	Arg	Met	Ala	Met	Ala	Phe	Ser	Leu	Ala	Ala	Cys	Ala	Asp	405	410	415	
Val	Pro	Val	Thr	Ile	Lys	Asp	Pro	Gly	Cys	Thr	Arg	Lys	Thr	Phe	Pro	420	425	430	
Asn	Tyr	Phe	Asp	Val	Leu	Gln	Gln	Tyr	Ser	Lys	His	435	440						

155

7

<210> 54
 <211> 444
 <212> PRT
 <213> Lycopersicon esculentum

<220>
 <221> UNSURE
 <222> (1)..(444)
 <223> Xaa = any

<400> 54

Lys	Pro	His	Glu	Ile	Val	Leu	Xaa	Pro	Ile	Lys	Asp	Ile	Ser	Gly	Thr
1				5					10					15	
Val	Lys	Leu	Pro	Gly	Ser	Lys	Ser	Leu	Ser	Asn	Arg	Ile	Leu	Leu	Leu
			20					25					30		
Ala	Ala	Leu	Ser	Glu	Gly	Arg	Thr	Val	Val	Asp	Asn	Leu	Leu	Ser	Ser
		35					40					45			
Asp	Asp	Ile	His	Tyr	Met	Leu	Gly	Ala	Leu	Lys	Thr	Leu	Gly	Leu	His
	50					55					60				
Val	Glu	Asp	Asp	Asn	Glu	Asn	Gln	Arg	Ala	Ile	Val	Glu	Gly	Cys	Gly
65					70					75				80	
Gly	Gln	Phe	Pro	Val	Gly	Lys	Lys	Ser	Glu	Glu	Glu	Ile	Gln	Leu	Phe
				85					90					95	
Leu	Gly	Asn	Ala	Gly	Thr	Ala	Met	Arg	Pro	Leu	Thr	Ala	Ala	Val	Thr
		100						105						110	
Val	Ala	Gly	Gly	His	Ser	Arg	Tyr	Val	Leu	Asp	Gly	Val	Pro	Arg	Met
		115					120					125			
Arg	Glu	Arg	Pro	Ile	Gly	Asp	Leu	Val	Asp	Gly	Leu	Lys	Gln	Leu	Gly
	130					135					140				
Ala	Glu	Val	Asp	Cys	Ser	Leu	Gly	Thr	Asn	Cys	Pro	Pro	Val	Arg	Ile
145					150					155					160
Val	Ser	Lys	Gly	Gly	Leu	Pro	Gly	Gly	Lys	Val	Lys	Leu	Ser	Gly	Ser
			165						170					175	
Ile	Ser	Ser	Gln	Tyr	Leu	Thr	Ala	Leu	Leu	Met	Ala	Ala	Pro	Leu	Ala
			180					185					190		
Leu	Gly	Asp	Val	Glu	Ile	Glu	Ile	Ile	Asp	Lys	Leu	Ile	Ser	Val	Pro
	195						200					205			
Tyr	Val	Glu	Met	Thr	Leu	Lys	Leu	Met	Glu	Arg	Phe	Gly	Val	Phe	Val
	210					215					220				

156

F

Glu His Ser Ser Gly Trp Asp Arg Phe Leu Val Lys Gly Gly Gln Lys
 225 230 235 240

Tyr Lys Ser Pro Gly Lys Ala Phe Val Glu Gly Asp Ala Ser Ser Ala
 245 250 255

Ser Tyr Phe Leu Ala Gly Ala Ala Val Thr Gly Gly Thr Val Thr Val
 260 265 270

Glu Gly Cys Gly Thr Ser Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
 275 280 285

Val Leu Glu Lys Met Gly Ala Glu Val Thr Trp Thr Glu Asn Ser Val
 290 295 300

Thr Val Lys Gly Pro Pro Arg Asn Ser Ser Gly Met Lys His Leu Arg
 305 310 315 320

Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
 325 330 335

Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Thr Ile Arg Asp Val
 340 345 350

Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Ile Ala Ile Cys Thr
 355 360 365

Glu Leu Arg Lys Leu Gly Ala Thr Val Val Glu Gly Ser Asp Tyr Cys
 370 375 380

Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Glu Ile Asp Thr Tyr
 385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp
 405 410 415

Val Pro Val Thr Ile Lys Asn Pro Gly Cys Thr Arg Lys Thr Phe Pro
 420 425 430

Asp Tyr Phe Glu Val Leu Gln Lys Tyr Ser Lys His
 435 440

<210> 55
 <211> 444
 <212> PRT
 <213> Petunia x hybrida

<400> 55

Lys Pro Ser Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser Gly Thr
 1 5 10 15

Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu

20					25					30						
Ala	Ala	Leu	Ser	Glu	Gly	Thr	Thr	Val	Val	Asp	Asn	Leu	Leu	Ser	Ser	
35					40					45						
Asp	Asp	Ile	His	Tyr	Met	Leu	Gly	Ala	Leu	Lys	Thr	Leu	Gly	Leu	His	
50					55					60						
Val	Glu	Glu	Asp	Ser	Ala	Asn	Gln	Arg	Ala	Val	Val	Glu	Gly	Cys	Gly	
65					70					75					80	
Gly	Leu	Phe	Pro	Val	Gly	Lys	Glu	Ser	Lys	Glu	Glu	Ile	Gln	Leu	Phe	
85					90					95						
Leu	Gly	Asn	Ala	Gly	Thr	Ala	Met	Arg	Pro	Leu	Thr	Ala	Ala	Val	Thr	
100					105					110						
Val	Ala	Gly	Gly	Asn	Ser	Arg	Tyr	Val	Leu	Asp	Gly	Val	Pro	Arg	Met	
115					120					125						
Arg	Glu	Arg	Pro	Ile	Ser	Asp	Leu	Val	Asp	Gly	Leu	Lys	Gln	Leu	Gly	
130					135					140						
Ala	Glu	Val	Asp	Cys	Phe	Leu	Gly	Thr	Lys	Cys	Pro	Pro	Val	Arg	Ile	
145					150					155					160	
Val	Ser	Lys	Gly	Gly	Leu	Pro	Gly	Gly	Lys	Val	Lys	Leu	Ser	Gly	Ser	
165					170					175						
Ile	Ser	Ser	Gln	Tyr	Leu	Thr	Ala	Leu	Leu	Met	Ala	Ala	Pro	Leu	Ala	
180					185					190						
Leu	Gly	Asp	Val	Glu	Ile	Glu	Ile	Ile	Asp	Lys	Leu	Ile	Ser	Val	Pro	
195					200					205						
Tyr	Val	Glu	Met	Thr	Leu	Lys	Leu	Met	Glu	Arg	Phe	Gly	Ile	Ser	Val	
210					215					220						
Glu	His	Ser	Ser	Ser	Trp	Asp	Arg	Phe	Phe	Val	Arg	Gly	Gly	Gln	Lys	
225					230					235					240	
Tyr	Lys	Ser	Pro	Gly	Lys	Ala	Phe	Val	Glu	Gly	Asp	Ala	Ser	Ser	Ala	
245					250					255						
Ser	Tyr	Phe	Leu	Ala	Gly	Ala	Ala	Val	Thr	Gly	Gly	Thr	Ile	Thr	Val	
260					265					270						
Glu	Gly	Cys	Gly	Thr	Asn	Ser	Leu	Gln	Gly	Asp	Val	Lys	Phe	Ala	Glu	
275					280					285						
Val	Leu	Glu	Lys	Met	Gly	Ala	Glu	Val	Thr	Trp	Thr	Glu	Asn	Ser	Val	
290					295					300						
Thr	Val	Lys	Gly	Pro	Pro	Arg	Ser	Ser	Ser	Gly	Arg	Lys	His	Leu	Arg	

305		310		315		320
Ala Ile Asp Val	Asn Met Asn Lys Met	Pro Asp Val	Ala Met Thr Leu			
	325	330	335			
Ala Val Val Ala	Leu Tyr Ala Asp Gly	Pro Thr Ala	Ile Arg Asp Val			
	340	345	350			
Ala Ser Trp Arg	Val Lys Glu Thr Glu	Arg Met Ile	Ala Ile Cys Thr			
	355	360	365			
Glu Leu Arg Lys	Leu Gly Ala Thr Val	Glu Glu Gly	Pro Asp Tyr Cys			
	370	375	380			
Ile Ile Thr Pro	Pro Glu Lys Leu Asn	Val Thr Asp	Ile Asp Thr Tyr			
	385	390	395	400		
Asp Asp His Arg	Met Ala Met Ala	Phe Ser Leu	Ala Ala Cys Ala Asp			
	405	410	415			
Val Pro Val Thr	Ile Asn Asp Pro	Gly Cys Thr	Arg Lys Thr Phe Pro			
	420	425	430			
Asn Tyr Phe Asp	Val Leu Gln Gln	Tyr Ser Lys	His			
	435	440				

<210> 56
 <211> 444
 <212> PRT
 <213> Zea mays

 <400> 56

Ala Gly Ala Glu	Glu Ile Val Leu	Gln Pro Ile	Lys Glu Ile	Ser Gly
1	5	10	15	
Thr Val Lys Leu	Pro Gly Ser Lys	Ser Leu Ser	Asn Arg Ile	Leu Leu
	20	25	30	
Leu Ala Ala Leu	Ser Glu Gly Thr	Thr Val Val	Asp Asn Leu	Leu Asn
	35	40	45	
Ser Glu Asp Val	His Tyr Met Leu	Gly Ala Leu	Arg Thr Leu	Gly Leu
	50	55	60	
Ser Val Glu Ala	Asp Lys Ala Ala	Lys Arg Ala	Val Val Val	Gly Cys
	65	70	75	80
Gly Gly Lys Phe	Pro Val Glu Asp	Ala Lys Glu	Glu Val Gln	Leu Phe
	85	90	95	
Leu Gly Asn Ala	Gly Thr Ala Met	Arg Pro Leu	Thr Ala Ala	Val Thr
	100	105	110	

Ala	Ala	Gly	Gly	Asn	Ala	Thr	Tyr	Val	Leu	Asp	Gly	Val	Pro	Arg	Met	115	120	125	
Arg	Glu	Arg	Pro	Ile	Gly	Asp	Leu	Val	Val	Gly	Leu	Lys	Gln	Leu	Gly	130	135	140	
Ala	Asp	Val	Asp	Cys	Phe	Leu	Gly	Thr	Asp	Cys	Pro	Pro	Val	Arg	Val	145	150	155	160
Asn	Gly	Ile	Gly	Gly	Leu	Pro	Gly	Gly	Lys	Val	Lys	Leu	Ser	Gly	Ser	165	170	175	
Ile	Ser	Ser	Gln	Tyr	Leu	Ser	Ala	Leu	Leu	Met	Ala	Ala	Pro	Leu	Pro	180	185	190	
Leu	Gly	Asp	Val	Glu	Ile	Glu	Ile	Ile	Asp	Lys	Leu	Ile	Ser	Ile	Pro	195	200	205	
Tyr	Val	Glu	Met	Thr	Leu	Arg	Leu	Met	Glu	Arg	Phe	Gly	Val	Lys	Ala	210	215	220	
Glu	His	Ser	Asp	Ser	Trp	Asp	Arg	Phe	Tyr	Ile	Lys	Gly	Gly	Gln	Lys	225	230	235	240
Tyr	Lys	Ser	Pro	Lys	Asn	Ala	Tyr	Val	Glu	Gly	Asp	Ala	Ser	Ser	Ala	245	250	255	
Ser	Tyr	Phe	Leu	Ala	Gly	Ala	Ala	Ile	Thr	Gly	Gly	Thr	Val	Thr	Val	260	265	270	
Glu	Gly	Cys	Gly	Thr	Thr	Ser	Leu	Gln	Gly	Asp	Val	Lys	Phe	Ala	Glu	275	280	285	
Val	Leu	Glu	Met	Met	Gly	Ala	Lys	Val	Thr	Trp	Thr	Glu	Thr	Ser	Val	290	295	300	
Thr	Val	Thr	Gly	Pro	Pro	Arg	Glu	Pro	Phe	Gly	Arg	Lys	His	Leu	Lys	305	310	315	320
Ala	Ile	Asp	Val	Asn	Met	Asn	Lys	Met	Pro	Asp	Val	Ala	Met	Thr	Leu	325	330	335	
Ala	Val	Val	Ala	Leu	Phe	Ala	Asp	Gly	Pro	Thr	Ala	Ile	Arg	Asp	Val	340	345	350	
Ala	Ser	Trp	Arg	Val	Lys	Glu	Thr	Glu	Arg	Met	Val	Ala	Ile	Arg	Thr	355	360	365	
Glu	Leu	Thr	Lys	Leu	Gly	Ala	Ser	Val	Glu	Glu	Gly	Pro	Asp	Tyr	Cys	370	375	380	
Ile	Ile	Thr	Pro	Pro	Glu	Lys	Leu	Asn	Val	Thr	Ala	Ile	Asp	Thr	Tyr	385	390	395	400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu
 405 410 415

Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
 420 425 430

Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
 435 440

<210> 57
 <211> 427
 <212> PRT
 <213> Salmonella gallinarum

<400> 57

Met Glu Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Ala Ile
 1 5 10 15

Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Ala
 20 25 30

Ala Leu Ala Cys Gly Lys Thr Val Leu Thr Asn Leu Leu Asp Ser Asp
 35 40 45

Asp Val Arg His Met Leu Asn Ala Leu Ser Ala Leu Gly Ile Asn Tyr
 50 55 60

Thr Leu Ser Ala Asp Arg Thr Arg Cys Asp Ile Thr Gly Asn Gly Gly
 65 70 75 80

Pro Leu Arg Ala Pro Gly Ala Leu Glu Leu Phe Leu Gly Asn Ala Gly
 85 90 95

Thr Ala Met Arg Pro Leu Ala Ala Ala Leu Cys Leu Gly Gln Asn Glu
 100 105 110

Ile Val Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly His
 115 120 125

Leu Val Asp Ser Leu Arg Gln Gly Gly Ala Asn Ile Asp Tyr Leu Glu
 130 135 140

Gln Glu Asn Tyr Pro Pro Leu Arg Leu Arg Gly Gly Phe Ile Gly Gly
 145 150 155 160

Asp Ile Glu Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu
 165 170 175

Leu Met Thr Ala Pro Leu Ala Pro Lys Asp Thr Ile Ile Arg Val Lys
 180 185 190

Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu Asn Leu Met
 195 200 205

1.61

A

Lys Thr Phe Gly Val Glu Ile Ala Asn His His Tyr Gln Gln Phe Val
 210 215 220
 Val Lys Gly Gly Gln Gln Tyr His Ser Pro Gly Arg Tyr Leu Val Glu
 225 230 235 240
 Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Gly Ala Ile Lys
 245 250 255
 Gly Gly Thr Val Lys Val Thr Gly Ile Gly Arg Lys Ser Met Gln Gly
 260 265 270
 Asp Ile Arg Phe Ala Asp Val Leu Glu Lys Met Gly Ala Thr Ile Thr
 275 280 285
 Trp Gly Asp Asp Phe Ile Ala Cys Thr Arg Gly Glu Leu His Ala Ile
 290 295 300
 Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr
 305 310 315 320
 Thr Ala Leu Phe Ala Lys Gly Thr Thr Thr Leu Arg Asn Ile Tyr Asn
 325 330 335
 Trp Arg Val Lys Glu Thr Asp Arg Leu Phe Ala Met Ala Thr Glu Leu
 340 345 350
 Arg Lys Val Gly Ala Glu Val Glu Glu Gly His Asp Tyr Ile Arg Ile
 355 360 365
 Thr Pro Pro Ala Lys Leu Gln His Ala Asp Ile Gly Thr Tyr Asn Asp
 370 375 380
 His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro
 385 390 395 400
 Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr
 405 410 415
 Phe Glu Gln Leu Ala Arg Met Ser Thr Pro Ala
 420 425

<210> 58
 <211> 427
 <212> PRT
 <213> Salmonella typhimurium

<400> 58

Met Glu Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Ala Ile
 1 5 10 15

Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Leu Ala

20					25					30						
Ala	Leu	Ala	Cys	Gly	Lys	Thr	Val	Leu	Thr	Asn	Leu	Leu	Asp	Ser	Asp	
35					40					45						
Asp	Val	Arg	His	Met	Leu	Asn	Ala	Leu	Ser	Ala	Leu	Gly	Ile	Asn	Tyr	
50					55					60						
Thr	Leu	Ser	Ala	Asp	Arg	Thr	Arg	Cys	Asp	Ile	Thr	Gly	Asn	Gly	Gly	
65					70					75					80	
Pro	Leu	Arg	Ala	Ser	Gly	Thr	Leu	Glu	Leu	Phe	Leu	Gly	Asn	Ala	Gly	
85					90					95						
Thr	Ala	Met	Arg	Pro	Leu	Ala	Ala	Ala	Leu	Cys	Leu	Gly	Gln	Asn	Glu	
100					105					110						
Ile	Val	Leu	Thr	Gly	Glu	Pro	Arg	Met	Lys	Glu	Arg	Pro	Ile	Gly	His	
115					120					125						
Leu	Val	Asp	Ser	Leu	Arg	Gln	Gly	Gly	Ala	Asn	Ile	Asp	Tyr	Leu	Glu	
130					135					140						
Gln	Glu	Asn	Tyr	Pro	Pro	Leu	Arg	Leu	Arg	Gly	Gly	Phe	Ile	Gly	Gly	
145					150					155					160	
Asp	Ile	Glu	Val	Asp	Gly	Ser	Val	Ser	Ser	Gln	Phe	Leu	Thr	Ala	Leu	
165					170					175						
Leu	Met	Thr	Ala	Pro	Leu	Ala	Pro	Glu	Asp	Thr	Ile	Ile	Arg	Val	Lys	
180					185					190						
Gly	Glu	Leu	Val	Ser	Lys	Pro	Tyr	Ile	Asp	Ile	Thr	Leu	Asn	Leu	Met	
195					200					205						
Lys	Thr	Phe	Gly	Val	Glu	Ile	Ala	Asn	His	His	Tyr	Gln	Gln	Phe	Val	
210					215					220						
Val	Lys	Gly	Gly	Gln	Gln	Tyr	His	Ser	Pro	Gly	Arg	Tyr	Leu	Val	Glu	
225					230					235					240	
Gly	Asp	Ala	Ser	Ser	Ala	Ser	Tyr	Phe	Leu	Ala	Ala	Gly	Gly	Ile	Lys	
245					250					255						
Gly	Gly	Thr	Val	Lys	Val	Thr	Gly	Ile	Gly	Gly	Lys	Ser	Met	Gln	Gly	
260					265					270						
Asp	Ile	Arg	Phe	Ala	Asp	Val	Leu	His	Lys	Met	Gly	Ala	Thr	Ile	Thr	
275					280					285						
Trp	Gly	Asp	Asp	Phe	Ile	Ala	Cys	Thr	Arg	Gly	Glu	Leu	His	Ala	Ile	
290					295					300						
Asp	Met	Asp	Met	Asn	His	Ile	Pro	Asp	Ala	Ala	Met	Thr	Ile	Ala	Thr	

305		310		315		320
Thr Ala Leu Phe	Ala Lys Gly Thr Thr	Thr Leu Arg Asn Ile Tyr Asn				
	325		330		335	
Trp Arg Val Lys	Glu Thr Asp Arg	Leu Phe Ala Met Ala Thr Glu Leu				
	340		345		350	
Arg Lys Val Gly	Ala Glu Val Glu Glu Gly His Asp Tyr Ile Arg Ile					
	355		360		365	
Thr Pro Pro Ala	Lys Leu Gln His Ala Asp Ile Gly Thr Tyr Asn Asp					
	370		375		380	
His Arg Met Ala	Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro					
	385		390		395	400
Val Thr Ile Leu	Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr					
	405		410		415	
Phe Glu Gln Leu	Ala Arg Met Ser Thr Pro Ala					
	420		425			

<210> 59
 <211> 427
 <212> PRT
 <213> Klebsiella pneumoniae

<400> 59

Met Glu Ser Leu	Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Thr Val	
1	5	10 15
Asn Leu Pro Gly	Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Ala	
	20	25 30
Ala Leu Ala Arg	Gly Thr Thr Val Leu Thr Asn Leu Leu Asp Ser Asp	
	35	40 45
Asp Val Arg His	Met Leu Asn Ala Leu Ser Ala Leu Gly Val His Tyr	
	50	55 60
Val Leu Ser Ser	Asp Arg Thr Arg Cys Glu Val Thr Gly Thr Gly Gly	
65	70	75 80
Pro Leu Gln Ala	Gly Ser Ala Leu Glu Leu Phe Leu Gly Asn Ala Gly	
	85	90 95
Thr Ala Met Arg	Pro Leu Ala Ala Ala Leu Cys Leu Gly Ser Asn Asp	
	100	105 110
Ile Val Leu Thr	Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly His	
	115	120 125

Leu Val Asp Ala Leu Arg Gln Gly Gly Ala Gln Ile Asp Tyr Leu Glu
 130 135 140
 Gln Glu Asn Tyr Pro Pro Leu Arg Leu Arg Gly Gly Phe Thr Gly Gly
 145 150 155 160
 Asp Val Glu Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu
 165 170 175
 Leu Met Ala Ser Pro Leu Ala Pro Gln Asp Thr Val Ile Ala Ile Lys
 180 185 190
 Gly Glu Leu Val Ser Arg Pro Tyr Ile Asp Ile Thr Leu His Leu Met
 195 200 205
 Lys Thr Phe Gly Val Glu Val Glu Asn Gln Ala Tyr Gln Arg Phe Ile
 210 215 220
 Val Arg Gly Asn Gln Gln Tyr Gln Ser Pro Gly Asp Tyr Leu Val Glu
 225 230 235 240
 Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Gly Ala Ile Lys
 245 250 255
 Gly Gly Thr Val Lys Val Thr Gly Ile Gly Arg Asn Ser Val Gln Gly
 260 265 270
 Asp Ile Arg Phe Ala Asp Val Leu Glu Lys Met Gly Ala Thr Val Thr
 275 280 285
 Trp Gly Glu Asp Tyr Ile Ala Cys Thr Arg Gly Glu Leu Asn Ala Ile
 290 295 300
 Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr
 305 310 315 320
 Ala Ala Leu Phe Ala Arg Gly Thr Thr Thr Leu Arg Asn Ile Tyr Asn
 325 330 335
 Trp Arg Val Lys Glu Thr Asp Arg Leu Phe Ala Met Ala Thr Glu Leu
 340 345 350
 Arg Lys Val Gly Ala Glu Val Glu Glu Gly Glu Asp Tyr Ile Arg Ile
 355 360 365
 Thr Pro Pro Leu Thr Leu Gln Phe Ala Glu Ile Gly Thr Tyr Asn Asp
 370 375 380
 His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro
 385 390 395 400
 Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr
 405 410 415

Phe Gly Gln Leu Ala Arg Ile Ser Thr Leu Ala
 420 425

<210> 60
 <211> 427
 <212> PRT
 <213> Yersinia enterocolitica

<400> 60

Met Leu Glu Ser Leu Thr Leu His Pro Ile Ala Leu Ile Asn Gly Thr
 1 5 10 15

Val Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Leu
 20 25 30

Ala Ala Leu Ala Glu Gly Thr Thr Gln Leu Asn Asn Leu Leu Asp Ser
 35 40 45

Asp Asp Ile Arg His Met Leu Asn Ala Leu Gln Ala Leu Gly Val Lys
 50 55 60

Tyr Arg Leu Ser Ala Asp Arg Thr Arg Cys Glu Val Asp Gly Leu Gly
 65 70 75 80

Gly Lys Leu Val Ala Glu Gln Pro Leu Glu Leu Phe Leu Gly Asn Ala
 85 90 95

Gly Thr Ala Met Arg Pro Leu Ala Ala Ala Leu Cys Leu Gly Lys Asn
 100 105 110

Asp Ile Val Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly
 115 120 125

His Leu Val Asp Ala Leu Arg Gln Gly Gly Ala Gln Ile Asp Tyr Leu
 130 135 140

Glu Gln Glu Asn Tyr Arg Arg Cys Ile Ala Gly Gly Phe Arg Gly Gly
 145 150 155 160

Lys Leu Thr Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu
 165 170 175

Leu Met Thr Ala Pro Leu Ala Glu Gln Asp Thr Glu Ile Gln Ile Gln
 180 185 190

Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu His Leu Met
 195 200 205

Lys Ala Phe Gly Val Asp Val Val His Glu Asn Tyr Gln Ile Phe His
 210 215 220

Ile Lys Gly Gly Gln Thr Tyr Arg Ser Pro Gly Ile Tyr Leu Val Glu
 225 230 235 240

1166

F

Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Ala Ala Ile Lys
 245 250 255
 Gly Gly Thr Val Arg Val Thr Gly Ile Gly Lys Gln Ser Val Gln Gly
 260 265 270
 Asp Thr Lys Phe Ala Asp Val Leu Glu Lys Met Gly Ala Lys Ile Ser
 275 280 285
 Trp Gly Asp Asp Tyr Ile Glu Cys Ser Arg Gly Glu Leu Gln Gly Ile
 290 295 300
 Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr
 305 310 315 320
 Thr Ala Leu Phe Ala Asp Gly Pro Thr Val Ile Arg Asn Ile Tyr Asn
 325 330 335
 Trp Arg Val Lys Glu Thr Asp Arg Leu Ser Ala Met Ala Thr Glu Leu
 340 345 350
 Arg Lys Val Gly Ala Glu Val Glu Glu Gly Gln Asp Tyr Ile Arg Val
 355 360 365
 Val Pro Pro Ala Gln Leu Ile Ala Ala Glu Ile Gly Thr Tyr Asn Asp
 370 375 380
 His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro
 385 390 395 400
 Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr
 405 410 415
 Phe Glu Gln Leu Ala Arg Leu Ser Gln Ile Ala
 420 425

<210> 61
 <211> 432
 <212> PRT
 <213> Haemophilus influenzae

<400> 61

Met Glu Lys Ile Thr Leu Ala Pro Ile Ser Ala Val Glu Gly Thr Ile
 1 5 10 15
 Asn Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ala Leu Leu Leu Ala
 20 25 30
 Ala Leu Ala Lys Gly Thr Thr Lys Val Thr Asn Leu Leu Asp Ser Asp
 35 40 45
 Asp Ile Arg His Met Leu Asn Ala Leu Lys Ala Leu Gly Val Arg Tyr

50					55					60					
Gln	Leu	Ser	Asp	Asp	Lys	Thr	Ile	Cys	Glu	Ile	Glu	Gly	Leu	Gly	Gly
65					70					75					80
Ala	Phe	Asn	Ile	Gln	Asp	Asn	Leu	Ser	Leu	Phe	Leu	Gly	Asn	Ala	Gly
				85					90					95	
Thr	Ala	Met	Arg	Pro	Leu	Thr	Ala	Ala	Leu	Cys	Leu	Lys	Gly	Asn	His
			100					105					110		
Glu	Val	Glu	Ile	Ile	Leu	Thr	Gly	Glu	Pro	Arg	Met	Lys	Glu	Arg	Pro
		115					120					125			
Ile	Leu	His	Leu	Val	Asp	Ala	Leu	Arg	Gln	Ala	Gly	Ala	Asp	Ile	Arg
		130				135					140				
Tyr	Leu	Glu	Asn	Glu	Gly	Tyr	Pro	Pro	Leu	Ala	Ile	Arg	Asn	Lys	Gly
145					150					155					160
Ile	Lys	Gly	Gly	Lys	Val	Lys	Ile	Asp	Gly	Ser	Ile	Ser	Ser	Gln	Phe
				165					170					175	
Leu	Thr	Ala	Leu	Leu	Met	Ser	Ala	Pro	Leu	Ala	Glu	Asn	Asp	Thr	Glu
			180					185					190		
Ile	Glu	Ile	Ile	Gly	Glu	Leu	Val	Ser	Lys	Pro	Tyr	Ile	Asp	Ile	Thr
		195					200					205			
Leu	Ala	Met	Met	Arg	Asp	Phe	Gly	Val	Lys	Val	Glu	Asn	His	His	Tyr
		210				215					220				
Gln	Lys	Phe	Gln	Val	Lys	Gly	Asn	Gln	Ser	Tyr	Ile	Ser	Pro	Asn	Lys
225					230					235					240
Tyr	Leu	Val	Glu	Gly	Asp	Ala	Ser	Ser	Ala	Ser	Tyr	Phe	Leu	Ala	Ala
				245					250					255	
Gly	Ala	Ile	Lys	Gly	Lys	Val	Lys	Val	Thr	Gly	Ile	Gly	Lys	Asn	Ser
			260					265					270		
Ile	Gln	Gly	Asp	Arg	Leu	Phe	Ala	Asp	Val	Leu	Glu	Lys	Met	Gly	Ala
		275					280					285			
Lys	Ile	Thr	Trp	Gly	Glu	Asp	Phe	Ile	Gln	Ala	Glu	His	Ala	Glu	Leu
		290				295					300				
Asn	Gly	Ile	Asp	Met	Asp	Met	Asn	His	Ile	Pro	Asp	Ala	Ala	Met	Thr
305					310					315					320
Ile	Ala	Thr	Thr	Ala	Leu	Phe	Ser	Asn	Gly	Glu	Thr	Val	Ile	Arg	Asn
				325					330					335	
Ile	Tyr	Asn	Trp	Arg	Val	Lys	Glu	Thr	Asp	Arg	Leu	Thr	Ala	Met	Ala

1108

7

340	345	350
Thr Glu Leu Arg Lys Val Gly Ala Glu Val Glu Glu Gly Glu Asp Phe		
355	360	365
Ile Arg Ile Gln Pro Leu Ala Leu Asn Gln Phe Lys His Ala Asn Ile		
370	375	380
Glu Thr Tyr Asn Asp His Arg Met Ala Met Cys Phe Ser Leu Ile Ala		
385	390	395 400
Leu Ser Asn Thr Pro Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys		
	405 410	415
Thr Phe Pro Thr Phe Phe Asn Glu Phe Glu Lys Ile Cys Leu Lys Asn		
	420 425	430
<210> 62		
<211> 441		
<212> PRT		
<213> Pasteurella multocida		
<400> 62		
Val Ile Lys Asp Ala Thr Ala Ile Thr Leu Asn Pro Ile Ser Tyr Ile		
1	5 10	15
Glu Gly Glu Val Arg Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ala		
	20 25	30
Leu Leu Leu Ser Ala Leu Ala Lys Gly Lys Thr Thr Leu Thr Asn Leu		
	35 40	45
Leu Asp Ser Asp Asp Val Arg His Met Leu Asn Ala Leu Lys Glu Leu		
	50 55	60
Gly Val Thr Tyr Gln Leu Ser Glu Asp Lys Ser Val Cys Glu Ile Glu		
65	70 75	80
Gly Leu Gly Arg Ala Phe Glu Trp Gln Ser Gly Leu Ala Leu Phe Leu		
	85 90	95
Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Leu Cys Leu		
	100 105	110
Ser Thr Pro Asn Arg Glu Gly Lys Asn Glu Ile Val Leu Thr Gly Glu		
	115 120	125
Pro Arg Met Lys Glu Arg Pro Ile Gln His Leu Val Asp Ala Leu Cys		
	130 135	140
Gln Ala Gly Ala Glu Ile Gln Tyr Leu Glu Gln Glu Gly Tyr Pro Pro		
145	150 155	160

Ile	Ala	Ile	Arg	Asn	Thr	Gly	Leu	Lys	Gly	Gly	Arg	Ile	Gln	Ile	Asp	165	170	175
Gly	Ser	Val	Ser	Ser	Gln	Phe	Leu	Thr	Ala	Leu	Leu	Met	Ala	Ala	Pro	180	185	190
Met	Ala	Glu	Ala	Asp	Thr	Glu	Ile	Glu	Ile	Ile	Gly	Glu	Leu	Val	Ser	195	200	205
Lys	Pro	Tyr	Ile	Asp	Ile	Thr	Leu	Lys	Met	Met	Gln	Thr	Phe	Gly	Val	210	215	220
Glu	Val	Glu	Asn	Gln	Ala	Tyr	Gln	Arg	Phe	Leu	Val	Lys	Gly	His	Gln	225	230	235
Gln	Tyr	Gln	Ser	Pro	His	Arg	Phe	Leu	Val	Glu	Gly	Asp	Ala	Ser	Ser	245	250	255
Ala	Ser	Tyr	Phe	Leu	Ala	Ala	Ala	Ala	Ile	Lys	Gly	Lys	Val	Lys	Val	260	265	270
Thr	Gly	Val	Gly	Lys	Asn	Ser	Ile	Gln	Gly	Asp	Arg	Leu	Phe	Ala	Asp	275	280	285
Val	Leu	Glu	Lys	Met	Gly	Ala	His	Ile	Thr	Trp	Gly	Asp	Asp	Phe	Ile	290	295	300
Gln	Val	Glu	Lys	Gly	Asn	Leu	Lys	Gly	Ile	Asp	Met	Asp	Met	Asn	His	305	310	315
Ile	Pro	Asp	Ala	Ala	Met	Thr	Ile	Ala	Thr	Thr	Ala	Leu	Phe	Ala	Glu	325	330	335
Gly	Glu	Thr	Val	Ile	Arg	Asn	Ile	Tyr	Asn	Trp	Arg	Val	Lys	Glu	Thr	340	345	350
Asp	Arg	Leu	Thr	Ala	Met	Ala	Thr	Glu	Leu	Arg	Lys	Val	Gly	Ala	Glu	355	360	365
Val	Glu	Glu	Gly	Glu	Asp	Phe	Ile	Arg	Ile	Gln	Pro	Leu	Asn	Leu	Ala	370	375	380
Gln	Phe	Gln	His	Ala	Glu	Leu	Asn	Ile	His	Asp	His	Arg	Met	Ala	Met	385	390	395
Cys	Phe	Ala	Leu	Ile	Ala	Leu	Ser	Lys	Thr	Ser	Val	Thr	Ile	Leu	Asp	405	410	415
Pro	Ser	Cys	Thr	Ala	Lys	Thr	Phe	Pro	Thr	Phe	Leu	Ile	Leu	Phe	Thr	420	425	430
Leu	Asn	Thr	Arg	Glu	Val	Ala	Tyr	Arg								435	440	

170

7

<210> 63
 <211> 426
 <212> PRT
 <213> Aeromonas salmonicida

<400> 63

Asn Ser Leu Arg Leu Glu Pro Ile Ser Arg Val Ala Gly Glu Val Asn
 1 5 10 15

Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Leu Ala Ala
 20 25 30

Leu Ala Arg Gly Thr Thr Arg Leu Thr Asn Leu Leu Asp Ser Asp Asp
 35 40 45

Ile Arg His Met Leu Ala Ala Leu Thr Gln Leu Gly Val Lys Tyr Lys
 50 55 60

Leu Ser Ala Asp Lys Thr Glu Cys Thr Val His Gly Leu Gly Arg Ser
 65 70 75 80

Phe Ala Val Ser Ala Pro Val Asn Leu Phe Leu Gly Asn Ala Gly Thr
 85 90 95

Ala Met Arg Pro Leu Cys Ala Ala Leu Cys Leu Gly Ser Gly Glu Tyr
 100 105 110

Met Leu Gly Gly Glu Pro Arg Met Glu Glu Arg Pro Ile Gly His Leu
 115 120 125

Val Asp Cys Leu Ala Leu Lys Gly Ala His Ile Gln Tyr Leu Lys Lys
 130 135 140

Asp Gly Tyr Pro Pro Leu Val Val Asp Ala Lys Gly Leu Trp Gly Gly
 145 150 155 160

Asp Val His Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Phe
 165 170 175

Leu Met Ala Ala Pro Ala Met Ala Pro Val Ile Pro Arg Ile His Ile
 180 185 190

Lys Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu His Ile
 195 200 205

Met Asn Ser Ser Gly Val Val Ile Glu His Asp Asn Tyr Lys Leu Phe
 210 215 220

Tyr Ile Lys Gly Asn Gln Ser Ile Val Ser Pro Gly Asp Phe Leu Val
 225 230 235 240

Glu Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Gly Ala Ile
 245 250 255

171

Lys Gly Lys Val Arg Val Thr Gly Ile Gly Lys His Ser Ile Gly Asp
260 265 270

Ile His Phe Ala Asp Val Leu Glu Arg Met Gly Ala Arg Ile Thr Trp
275 280 285

Gly Asp Asp Phe Ile Glu Ala Glu Gln Gly Pro Leu His Gly Val Asp
290 295 300

Met Asp Met Asn His Ile Pro Asp Val Gly His Asp His Ser Gly Gln
305 310 315 320

Ser His Cys Leu Pro Arg Val Pro Pro His Ser Gln His Leu Gln Leu
325 330 335

Ala Val Arg Asp Asp Arg Cys Thr Pro Cys Thr His Gly His Arg Arg
340 345 350

Ala Gln Ala Gly Val Ser Glu Glu Gly Thr Thr Phe Ile Thr Arg Asp
355 360 365

Ala Ala Asp Pro Ala Gln Ala Arg Arg Asp Arg His Leu Gln Arg Ser
370 375 380

Arg Ile Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Ile Ala Val
385 390 395 400

Thr Ile Asn Asp Pro Gly Cys Thr Ser Lys Thr Phe Pro Asp Tyr Phe
405 410 415

Asp Lys Leu Ala Ser Val Ser Gln Ala Val
420 425

<210> 64

<211> 442

<212> PRT

<213> Bacillus pertussis

<400> 64

Met Ser Gly Leu Ala Tyr Leu Asp Leu Pro Ala Ala Arg Leu Ala Arg
1 5 10 15

Gly Glu Val Ala Leu Pro Gly Ser Lys Ser Ile Ser Asn Arg Val Leu
20 25 30

Leu Leu Ala Ala Leu Ala Glu Gly Ser Thr Glu Ile Thr Gly Leu Leu
35 40 45

Asp Ser Asp Asp Thr Arg Val Met Leu Ala Ala Leu Arg Gln Leu Gly
50 55 60

Val Ser Val Gly Glu Val Ala Asp Gly Cys Val Thr Ile Glu Gly Val

65		70		75		80
Ala Arg Phe Pro Thr Glu Gln Ala Glu Leu Phe Leu Gly Asn Ala Gly						
	85			90		95
Thr Ala Phe Arg Pro Leu Thr Ala Ala Leu Ala Leu Met Gly Gly Asp						
	100			105		110
Tyr Arg Leu Ser Gly Val Pro Arg Met His Glu Arg Pro Ile Gly Asp						
	115			120		125
Leu Val Asp Ala Leu Arg Gln Phe Gly Ala Gly Ile Glu Tyr Leu Gly						
	130			135		140
Gln Ala Gly Tyr Pro Pro Leu Arg Ile Gly Gly Gly Ser Ile Arg Val						
	145			150		155
Asp Gly Pro Val Arg Val Glu Gly Ser Val Ser Ser Gln Phe Leu Thr						
	165			170		175
Ala Leu Leu Met Ala Ala Pro Val Leu Ala Arg Arg Ser Gly Gln Asp						
	180			185		190
Ile Thr Ile Glu Val Val Gly Glu Leu Ile Ser Lys Pro Tyr Ile Glu						
	195			200		205
Ile Thr Leu Asn Leu Met Ala Arg Phe Gly Val Ser Val Arg Arg Asp						
	210			215		220
Gly Trp Arg Ala Phe Thr Ile Ala Arg Asp Ala Val Tyr Arg Gly Pro						
	225			230		235
Gly Arg Met Ala Ile Glu Gly Asp Ala Ser Thr Ala Ser Tyr Phe Leu						
	245			250		255
Ala Leu Gly Ala Ile Gly Gly Gly Pro Val Arg Val Thr Gly Val Gly						
	260			265		270
Glu Asp Ser Ile Gln Gly Asp Val Ala Phe Ala Ala Thr Leu Ala Ala						
	275			280		285
Met Gly Ala Asp Val Arg Tyr Gly Pro Gly Trp Ile Glu Thr Arg Gly						
	290			295		300
Val Arg Val Ala Glu Gly Gly Arg Leu Lys Ala Phe Asp Ala Asp Phe						
	305			310		315
Asn Leu Ile Pro Asp Ala Ala Met Thr Ala Ala Thr Leu Ala Leu Tyr						
	325			330		335
Ala Asp Gly Pro Cys Arg Leu Arg Asn Ile Gly Ser Trp Arg Val Lys						
	340			345		350
Glu Thr Asp Arg Ile His Ala Met His Thr Glu Leu Glu Lys Leu Gly						

173

7

355

360

365

Ala Gly Val Gln Ser Gly Ala Asp Trp Leu Glu Val Ala Pro Pro Glu
370 375 380

Pro Gly Gly Trp Arg Asp Ala His Ile Gly Thr Trp Asp Asp His Arg
385 390 395 400

Met Ala Met Cys Phe Leu Leu Ala Ala Phe Gly Pro Ala Ala Val Arg
405 410 415

Ile Leu Asp Pro Gly Cys Val Ser Lys Thr Phe Pro Asp Tyr Phe Asp
420 425 430

Val Tyr Ala Gly Leu Leu Ala Ala Arg Asp
435 440

<210> 65

<211> 427

<212> PRT

<213> Salmonella typhimurium

<400> 65

Met Glu Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Ala Ile
1 5 10 15

Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Ala
20 25 30

Ala Leu Ala Cys Gly Lys Thr Val Leu Thr Asn Leu Leu Asp Ser Asp
35 40 45

Asp Val Arg His Met Leu Asn Ala Leu Ser Ala Leu Gly Ile Asn Tyr
50 55 60

Thr Leu Ser Ala Asp Arg Thr Arg Cys Asp Ile Thr Gly Asn Gly Gly
65 70 75 80

Pro Leu Arg Ala Ser Gly Thr Leu Glu Leu Phe Leu Gly Asn Ala Gly
85 90 95

Thr Ala Met Arg Pro Leu Ala Ala Ala Leu Cys Leu Gly Gln Asn Glu
100 105 110

Ile Val Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly His
115 120 125

Leu Val Asp Ser Leu Arg Gln Gly Gly Ala Asn Ile Asp Tyr Leu Glu
130 135 140

Gln Glu Asn Tyr Pro Pro Leu Arg Leu Arg Gly Gly Phe Ile Gly Gly
145 150 155 160

Asp	Ile	Glu	Val	Asp	Gly	Ser	Val	Ser	Ser	Gln	Phe	Leu	Thr	Ala	Leu	165	170	175
Leu	Met	Thr	Ala	Pro	Leu	Ala	Pro	Glu	Asp	Thr	Ile	Ile	Arg	Val	Lys	180	185	190
Gly	Glu	Leu	Val	Ser	Lys	Pro	Tyr	Ile	Asp	Ile	Thr	Leu	Asn	Leu	Met	195	200	205
Lys	Thr	Phe	Gly	Val	Glu	Ile	Ala	Asn	His	His	Tyr	Gln	Gln	Phe	Val	210	215	220
Val	Lys	Gly	Gly	Gln	Gln	Tyr	His	Ser	Pro	Gly	Arg	Tyr	Leu	Val	Glu	225	230	235
Gly	Asp	Ala	Ser	Ser	Ala	Ser	Tyr	Phe	Leu	Ala	Ala	Gly	Gly	Ile	Lys	245	250	255
Gly	Gly	Thr	Val	Lys	Val	Thr	Gly	Ile	Gly	Gly	Lys	Ser	Met	Gln	Gly	260	265	270
Asp	Ile	Arg	Phe	Ala	Asp	Val	Leu	His	Lys	Met	Gly	Ala	Thr	Ile	Thr	275	280	285
Trp	Gly	Asp	Asp	Phe	Ile	Ala	Cys	Thr	Arg	Gly	Glu	Leu	His	Ala	Ile	290	295	300
Asp	Met	Asp	Met	Asn	His	Ile	Pro	Asp	Ala	Ala	Met	Thr	Ile	Ala	Thr	305	310	315
Thr	Ala	Leu	Phe	Ala	Lys	Gly	Thr	Thr	Thr	Leu	Arg	Asn	Ile	Tyr	Asn	325	330	335
Trp	Arg	Val	Lys	Glu	Thr	Asp	Arg	Leu	Phe	Ala	Met	Ala	Thr	Glu	Leu	340	345	350
Arg	Lys	Val	Gly	Ala	Glu	Val	Glu	Glu	Gly	His	Asp	Tyr	Ile	Arg	Ile	355	360	365
Thr	Pro	Pro	Ala	Lys	Leu	Gln	His	Ala	Asp	Ile	Gly	Thr	Tyr	Asn	Asp	370	375	380
His	Arg	Met	Ala	Met	Cys	Phe	Ser	Leu	Val	Ala	Leu	Ser	Asp	Thr	Pro	385	390	395
Val	Thr	Ile	Leu	Asp	Pro	Lys	Cys	Thr	Ala	Lys	Thr	Phe	Pro	Asp	Tyr	405	410	415
Phe	Glu	Gln	Leu	Ala	Arg	Met	Ser	Thr	Pro	Ala						420	425	

<210> 66
 <211> 1894
 <212> DNA

115

F

<213> Synechocystis sp.

<220>

<221> CDS

<222> (275)..(1618)

<400> 66

acgggctgta acggtagtag ggggtcccgag cacaaaagcg gtgccggcaa gcagaactaa	60
tttccatggg gaataatggt atttcattgg tttggcctct ggtctggcaa tggttgctag	120
gcgatcgctt gttgaaatta acaaactgtc gcccttccac tgaccatggt aacgatgttt	180
tttacttctt tgactaaccg aggaaaattt ggcggggggc agaaatgcc aatacaattta	240
gcttgggtctt ccctgcccct aatttgtccc ctcc atg gcc ttg ctt tcc ctc aac	295
Met Ala Leu Leu Ser Leu Asn	
1 5	
aat cat caa tcc cat caa cgc tta act gtt aat ccc cct gcc caa ggg	343
Asn His Gln Ser His Gln Arg Leu Thr Val Asn Pro Pro Ala Gln Gly	
10 15 20	
gtc gct ttg act ggc cgc cta agg gtg ccg ggg gat aaa tcc att tcc	391
Val Ala Leu Thr Gly Arg Leu Arg Val Pro Gly Asp Lys Ser Ile Ser	
25 30 35	
cat cgg gcc ttg atg ttg ggg gcg atc gcc acc ggg gaa acc att atc	439
His Arg Ala Leu Met Leu Gly Ala Ile Ala Thr Gly Glu Thr Ile Ile	
40 45 50 55	
gaa ggg cta ctg ttg ggg gaa gat ccc cgt agt acg gcc cat tgc ttt	487
Glu Gly Leu Leu Leu Gly Glu Asp Pro Arg Ser Thr Ala His Cys Phe	
60 65 70	
cgg gcc atg gga gca gaa atc agc gaa cta aat tca gaa aaa atc atc	535
Arg Ala Met Gly Ala Glu Ile Ser Glu Leu Asn Ser Glu Lys Ile Ile	
75 80 85	
gtt cag ggt cgg ggt ctg gga cag ttg cag gaa ccc agt acc gtt ttg	583
Val Gln Gly Arg Gly Leu Gly Gln Leu Gln Glu Pro Ser Thr Val Leu	
90 95 100	
gat gcg ggg aac tct ggc acc acc atg cgc tta atg ttg ggc ttg cta	631
Asp Ala Gly Asn Ser Gly Thr Thr Met Arg Leu Met Leu Gly Leu Leu	
105 110 115	
gcc ggg caa aaa gat tgt tta ttc acc gtc acc ggc gat gat tcc ctc	679
Ala Gly Gln Lys Asp Cys Leu Phe Thr Val Thr Gly Asp Asp Ser Leu	
120 125 130 135	
cgt cac cgc ccc atg tcc cgg gta att caa ccc ttg caa caa atg ggg	727
Arg His Arg Pro Met Ser Arg Val Ile Gln Pro Leu Gln Gln Met Gly	
140 145 150	

gca aaa att tgg gcc cgg agt aac ggc aag ttt gcg ccg ctg gca gtc	775
Ala Lys Ile Trp Ala Arg Ser Asn Gly Lys Phe Ala Pro Leu Ala Val	
155 160 165	
cag ggt agc caa tta aaa ccg atc cat tac cat tcc ccc att gct tca	823
Gln Gly Ser Gln Leu Lys Pro Ile His Tyr His Ser Pro Ile Ala Ser	
170 175 180	
gcc cag gta aag tcc tgc ctg ttg cta gcg ggg tta acc acc gag ggg	871
Ala Gln Val Lys Ser Cys Leu Leu Leu Ala Gly Leu Thr Thr Glu Gly	
185 190 195	
gac acc acg gtt aca gaa cca gct cta tcc cgg gat cat agc gaa cgc	919
Asp Thr Thr Val Thr Glu Pro Ala Leu Ser Arg Asp His Ser Glu Arg	
200 205 210 215	
atg ttg cag gcc ttt gga gcc aaa tta acc att gat cca gta acc cat	967
Met Leu Gln Ala Phe Gly Ala Lys Leu Thr Ile Asp Pro Val Thr His	
220 225 230	
agc gtc act gtc cat ggc ccg gcc cat tta acg ggg caa cgg gtg gtg	1015
Ser Val Thr Val His Gly Pro Ala His Leu Thr Gly Gln Arg Val Val	
235 240 245	
gtg cca ggg gac atc agc tcg gcg gcc ttt tgg tta gtg gcg gca tcc	1063
Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Trp Leu Val Ala Ala Ser	
250 255 260	
att ttg cct gga tca gaa ttg ttg gtg gaa aat gta ggc att aac ccc	1111
Ile Leu Pro Gly Ser Glu Leu Leu Val Glu Asn Val Gly Ile Asn Pro	
265 270 275	
acc agg aca ggg gtg ttg gaa gtg ttg gcc cag atg ggg gcg gac att	1159
Thr Arg Thr Gly Val Leu Glu Val Leu Ala Gln Met Gly Ala Asp Ile	
280 285 290 295	
acc ccg gag aat gaa cga ttg gta acg ggg gaa ccg gta gca gat ctg	1207
Thr Pro Glu Asn Glu Arg Leu Val Thr Gly Glu Pro Val Ala Asp Leu	
300 305 310	
cgg gtt agg gca agc cat ctc cag ggt tgc acc ttc ggc ggc gaa att	1255
Arg Val Arg Ala Ser His Leu Gln Gly Cys Thr Phe Gly Gly Glu Ile	
315 320 325	
att ccc cga ctg att gat gaa att ccc att ttg gca gtg gcg gcg gcc	1303
Ile Pro Arg Leu Ile Asp Glu Ile Pro Ile Leu Ala Val Ala Ala Ala	
330 335 340	
ttt gca gag ggc act acc cgc att gaa gat gcc gca gaa ctg agg gtt	1351
Phe Ala Glu Gly Thr Thr Arg Ile Glu Asp Ala Ala Glu Leu Arg Val	
345 350 355	
aaa gaa agc gat cgc ctg gcg gcc att gct tcg gag ttg ggc aaa atg	1399

Lys Glu Ser Asp Arg Leu Ala Ala Ile Ala Ser Glu Leu Gly Lys Met
 360 365 370 375
 ggg gcc aaa gtc acc gaa ttt gat gat ggc ctg gaa att caa ggg gga 1447
 Gly Ala Lys Val Thr Glu Phe Asp Asp Gly Leu Glu Ile Gln Gly Gly
 380 385 390
 agc ccg tta caa ggg gcc gag gtg gat agc ttg acg gat cat cgc att 1495
 Ser Pro Leu Gln Gly Ala Glu Val Asp Ser Leu Thr Asp His Arg Ile
 395 400 405
 gcc atg gcg ttg gcg atc gcc gct tta ggt agt ggg ggg caa aca att 1543
 Ala Met Ala Leu Ala Ile Ala Ala Leu Gly Ser Gly Gly Gln Thr Ile
 410 415 420
 att aac cgg gcg gaa gcg gcc gcc att tcc tat cca gaa ttt ttt ggc 1591
 Ile Asn Arg Ala Glu Ala Ala Ala Ile Ser Tyr Pro Glu Phe Phe Gly
 425 430 435
 acg cta ggg caa gtt gcc caa gga taa agttagaaaa actcctgggc 1638
 Thr Leu Gly Gln Val Ala Gln Gly
 440 445
 ggtttgtaaa tgttttacca aggtagtttg gggttaaaggc cccagcaagt gctgccaggg 1698
 taatttatcc gcaattgacc aatcggcattg gaccgtatcg ttcaaactgg gtaattctcc 1758
 ctttaattcc ttaaaagctc gcttaaaaact gcccaacgta tctccgtaat ggcgagtgag 1818
 tagaagtaat ggggccaaac ggcgatcgcc acgggaaatt aaagcctgca tcaactgacca 1878
 cttataactt tcggga 1894

<210> 67
 <211> 447
 <212> PRT
 <213> Synechocystis sp.

<400> 67

Met Ala Leu Leu Ser Leu Asn Asn His Gln Ser His Gln Arg Leu Thr
 1 5 10 15

Val Asn Pro Pro Ala Gln Gly Val Ala Leu Thr Gly Arg Leu Arg Val
 20 25 30

Pro Gly Asp Lys Ser Ile Ser His Arg Ala Leu Met Leu Gly Ala Ile
 35 40 45

Ala Thr Gly Glu Thr Ile Ile Glu Gly Leu Leu Leu Gly Glu Asp Pro

50

55

60

Arg Ser Thr Ala His Cys Phe Arg Ala Met Gly Ala Glu Ile Ser Glu
65 70 75 80

Leu Asn Ser Glu Lys Ile Ile Val Gln Gly Arg Gly Leu Gly Gln Leu
85 90 95

Gln Glu Pro Ser Thr Val Leu Asp Ala Gly Asn Ser Gly Thr Thr Met
100 105 110

Arg Leu Met Leu Gly Leu Leu Ala Gly Gln Lys Asp Cys Leu Phe Thr
115 120 125

Val Thr Gly Asp Asp Ser Leu Arg His Arg Pro Met Ser Arg Val Ile
130 135 140

Gln Pro Leu Gln Gln Met Gly Ala Lys Ile Trp Ala Arg Ser Asn Gly
145 150 155 160

Lys Phe Ala Pro Leu Ala Val Gln Gly Ser Gln Leu Lys Pro Ile His
165 170 175

Tyr His Ser Pro Ile Ala Ser Ala Gln Val Lys Ser Cys Leu Leu Leu
180 185 190

Ala Gly Leu Thr Thr Glu Gly Asp Thr Thr Val Thr Glu Pro Ala Leu
195 200 205

Ser Arg Asp His Ser Glu Arg Met Leu Gln Ala Phe Gly Ala Lys Leu
210 215 220

Thr Ile Asp Pro Val Thr His Ser Val Thr Val His Gly Pro Ala His
225 230 235 240

Leu Thr Gly Gln Arg Val Val Val Pro Gly Asp Ile Ser Ser Ala Ala
245 250 255

Phe Trp Leu Val Ala Ala Ser Ile Leu Pro Gly Ser Glu Leu Leu Val
260 265 270

Glu Asn Val Gly Ile Asn Pro Thr Arg Thr Gly Val Leu Glu Val Leu
 275 280 285

Ala Gln Met Gly Ala Asp Ile Thr Pro Glu Asn Glu Arg Leu Val Thr
 290 295 300

Gly Glu Pro Val Ala Asp Leu Arg Val Arg Ala Ser His Leu Gln Gly
 305 310 315 320

Cys Thr Phe Gly Gly Glu Ile Ile Pro Arg Leu Ile Asp Glu Ile Pro
 325 330 335

Ile Leu Ala Val Ala Ala Ala Phe Ala Glu Gly Thr Thr Arg Ile Glu
 340 345 350

Asp Ala Ala Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Ile
 355 360 365

Ala Ser Glu Leu Gly Lys Met Gly Ala Lys Val Thr Glu Phe Asp Asp
 370 375 380

Gly Leu Glu Ile Gln Gly Gly Ser Pro Leu Gln Gly Ala Glu Val Asp
 385 390 395 400

Ser Leu Thr Asp His Arg Ile Ala Met Ala Leu Ala Ile Ala Ala Leu
 405 410 415

Gly Ser Gly Gly Gln Thr Ile Ile Asn Arg Ala Glu Ala Ala Ala Ile
 420 425 430

Ser Tyr Pro Glu Phe Phe Gly Thr Leu Gly Gln Val Ala Gln Gly
 435 440 445

<210> 68
 <211> 1479
 <212> DNA
 <213> Dichelobacter nodosus

<220>
 <221> CDS
 <222> (107) .. (1438)

180

A

<400> 68
 tttaaaaaca atgagttaaa aaattatattt tctggcacac gcgctttttt tgcatttttt 60
 ctcccatttt tccggcacaa taacgttggt ttataaaaag gaaatg atg atg acg 115
 Met Met Thr
 1
 aat ata tgg cac acc gcg ccc gtc tct gcg ctt tcc ggc gaa ata acg 163
 Asn Ile Trp His Thr Ala Pro Val Ser Ala Leu Ser Gly Glu Ile Thr
 5 10 15
 ata tgc ggc gat aaa tca atg tgc cat cgc gcc tta tta tta gca gcg 211
 Ile Cys Gly Asp Lys Ser Met Ser His Arg Ala Leu Leu Leu Ala Ala
 20 25 30 35
 tta gca gaa gga caa acg gaa atc cgc ggc ttt tta gcg tgc gcg gat 259
 Leu Ala Glu Gly Gln Thr Glu Ile Arg Gly Phe Leu Ala Cys Ala Asp
 40 45 50
 tgt ttg gcg acg cgg caa gca ttg cgc gca tta ggc gtt gat att caa 307
 Cys Leu Ala Thr Arg Gln Ala Leu Arg Ala Leu Gly Val Asp Ile Gln
 55 60 65
 aga gaa aaa gaa ata gtg acg att cgc ggt gtg gga ttt ctg ggt ttg 355
 Arg Glu Lys Glu Ile Val Thr Ile Arg Gly Val Gly Phe Leu Gly Leu
 70 75 80
 cag ccg ccg aaa gca ccg tta aat atg caa aac agt ggc act agc atg 403
 Gln Pro Pro Lys Ala Pro Leu Asn Met Gln Asn Ser Gly Thr Ser Met
 85 90 95
 cgt tta ttg gca gga att ttg gca gcg cag cgc ttt gag agc gtg tta 451
 Arg Leu Leu Ala Gly Ile Leu Ala Ala Gln Arg Phe Glu Ser Val Leu
 100 105 110 115
 tgc ggc gat gaa tca tta gaa aaa cgt ccg atg cag cgc att att acg 499
 Cys Gly Asp Glu Ser Leu Glu Lys Arg Pro Met Gln Arg Ile Ile Thr
 120 125 130
 ccg ctt gtg caa atg ggg gca aaa att gtc agt cac agc aat ttt acg 547
 Pro Leu Val Gln Met Gly Ala Lys Ile Val Ser His Ser Asn Phe Thr
 135 140 145
 gcg ccg tta cat att tca gga cgc ccg ctg acc ggc att gat tac gcg 595
 Ala Pro Leu His Ile Ser Gly Arg Pro Leu Thr Gly Ile Asp Tyr Ala
 150 155 160
 tta ccg ctt ccc agc gcg caa tta aaa agt tgc ctt att ttg gca gga 643
 Leu Pro Leu Pro Ser Ala Gln Leu Lys Ser Cys Leu Ile Leu Ala Gly
 165 170 175
 tta ttg gct gac ggt acc acg ccg ctg cat act tgc ggc atc agt cgc 691
 Leu Leu Ala Asp Gly Thr Thr Arg Leu His Thr Cys Gly Ile Ser Arg
 180 185 190 195

181

A

gac cac acg gaa cgc atg ttg ccg ctt ttt ggt ggc gca ctt gag atc	739
Asp His Thr Glu Arg Met Leu Pro Leu Phe Gly Gly Ala Leu Glu Ile	
200 205 210	
aag aaa gag caa ata atc gtc acc ggt gga caa aaa ttg cac ggt tgc	787
Lys Lys Glu Gln Ile Ile Val Thr Gly Gly Gln Lys Leu His Gly Cys	
215 220 225	
gtg ctt gat att gtc ggc gat ttg tcg gcg gcg gcg ttt ttt atg gtt	835
Val Leu Asp Ile Val Gly Asp Leu Ser Ala Ala Ala Phe Phe Met Val	
230 235 240	
gcg gct ttg att gcg ccg cgc gcg gaa gtc gtt att cgt aat gtc ggc	883
Ala Ala Leu Ile Ala Pro Arg Ala Glu Val Val Ile Arg Asn Val Gly	
245 250 255	
att aat ccg acg cgg gcg gca atc att act ttg ttg caa aaa atg ggc	931
Ile Asn Pro Thr Arg Ala Ala Ile Ile Thr Leu Leu Gln Lys Met Gly	
260 265 270 275	
gga cgg att gaa ttg cat cat cag cgc ttt tgg ggc gcc gaa ccg gtg	979
Gly Arg Ile Glu Leu His His Gln Arg Phe Trp Gly Ala Glu Pro Val	
280 285 290	
gca gat att gtt gtt tat cat tca aaa ttg cgc ggc att acg gtg gcg	1027
Ala Asp Ile Val Val Tyr His Ser Lys Leu Arg Gly Ile Thr Val Ala	
295 300 305	
ccg gaa tgg att gcc aac gcg att gat gaa ttg ccg att ttt ttt att	1075
Pro Glu Trp Ile Ala Asn Ala Ile Asp Glu Leu Pro Ile Phe Phe Ile	
310 315 320	
gcg gca gct tgc gcg gaa ggg acg act ttt gtg ggc aat ttg tca gaa	1123
Ala Ala Ala Cys Ala Glu Gly Thr Thr Phe Val Gly Asn Leu Ser Glu	
325 330 335	
ttg cgt gtg aaa gaa tcg gat cgt tta gcg gcg atg gcg caa aat tta	1171
Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Met Ala Gln Asn Leu	
340 345 350 355	
caa act ttg ggc gtg gcg tgc gac gtt ggc gcc gat ttt att cat ata	1219
Gln Thr Leu Gly Val Ala Cys Asp Val Gly Ala Asp Phe Ile His Ile	
360 365 370	
tat gga aga agc gat ccg caa ttt tta ccg gcg ccg gtg aac agt ttt	1267
Tyr Gly Arg Ser Asp Arg Gln Phe Leu Pro Ala Arg Val Asn Ser Phe	
375 380 385	
ggc gat cat ccg att gcg atg agt ttg gcg gtg gca ggt gtg cgc gcg	1315
Gly Asp His Arg Ile Ala Met Ser Leu Ala Val Ala Gly Val Arg Ala	
390 395 400	
gca ggt gaa tta ttg att gat gac ggc gcg gtg gcg gcg gtt tct atg	1363

Ala Gly Glu Leu Leu Ile Asp Asp Gly Ala Val Ala Ala Val Ser Met
 405 410 415

ccg caa ttt cgc gat ttt gcc gcc gca att ggt atg aat gta gga gaa 1411
 Pro Gln Phe Arg Asp Phe Ala Ala Ala Ile Gly Met Asn Val Gly Glu
 420 425 430 435

aaa gat gcg aaa aat tgt cac gat tga tggctcctagc ggtgttgga 1458
 Lys Asp Ala Lys Asn Cys His Asp
 440

aaggcacggt ggcgcaagct t 1479

<210> 69
 <211> 443
 <212> PRT
 <213> Dichelobacter nodosus

<400> 69

Met Met Thr Asn Ile Trp His Thr Ala Pro Val Ser Ala Leu Ser Gly
 1 5 10 15

Glu Ile Thr Ile Cys Gly Asp Lys Ser Met Ser His Arg Ala Leu Leu
 20 25 30

Leu Ala Ala Leu Ala Glu Gly Gln Thr Glu Ile Arg Gly Phe Leu Ala
 35 40 45

Cys Ala Asp Cys Leu Ala Thr Arg Gln Ala Leu Arg Ala Leu Gly Val
 50 55 60

Asp Ile Gln Arg Glu Lys Glu Ile Val Thr Ile Arg Gly Val Gly Phe
 65 70 75 80

Leu Gly Leu Gln Pro Pro Lys Ala Pro Leu Asn Met Gln Asn Ser Gly
 85 90 95

Thr Ser Met Arg Leu Leu Ala Gly Ile Leu Ala Ala Gln Arg Phe Glu
 100 105 110

Ser Val Leu Cys Gly Asp Glu Ser Leu Glu Lys Arg Pro Met Gln Arg
 115 120 125

Ile Ile Thr Pro Leu Val Gln Met Gly Ala Lys Ile Val Ser His Ser

130		135		140
Asn Phe Thr Ala Pro Leu His Ile Ser Gly Arg Pro Leu Thr Gly Ile				
145		150	155	160
Asp Tyr Ala Leu Pro Leu Pro Ser Ala Gln Leu Lys Ser Cys Leu Ile				
	165		170	175
Leu Ala Gly Leu Leu Ala Asp Gly Thr Thr Arg Leu His Thr Cys Gly				
	180		185	190
Ile Ser Arg Asp His Thr Glu Arg Met Leu Pro Leu Phe Gly Gly Ala				
	195		200	205
Leu Glu Ile Lys Lys Glu Gln Ile Ile Val Thr Gly Gly Gln Lys Leu				
	210		215	220
His Gly Cys Val Leu Asp Ile Val Gly Asp Leu Ser Ala Ala Ala Phe				
	225		230	235
Phe Met Val Ala Ala Leu Ile Ala Pro Arg Ala Glu Val Val Ile Arg				
		245	250	255
Asn Val Gly Ile Asn Pro Thr Arg Ala Ala Ile Ile Thr Leu Leu Gln				
	260		265	270
Lys Met Gly Gly Arg Ile Glu Leu His His Gln Arg Phe Trp Gly Ala				
	275		280	285
Glu Pro Val Ala Asp Ile Val Val Tyr His Ser Lys Leu Arg Gly Ile				
	290		295	300
Thr Val Ala Pro Glu Trp Ile Ala Asn Ala Ile Asp Glu Leu Pro Ile				
	305		310	315
Phe Phe Ile Ala Ala Ala Cys Ala Glu Gly Thr Thr Phe Val Gly Asn				
		325	330	335
Leu Ser Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Met Ala				
	340		345	350

Gln Asn Leu Gln Thr Leu Gly Val Ala Cys Asp Val Gly Ala Asp Phe
355 360 365

Ile His Ile Tyr Gly Arg Ser Asp Arg Gln Phe Leu Pro Ala Arg Val
370 375 380

Asn Ser Phe Gly Asp His Arg Ile Ala Met Ser Leu Ala Val Ala Gly
385 390 395 400

Val Arg Ala Ala Gly Glu Leu Leu Ile Asp Asp Gly Ala Val Ala Ala
405 410 415

Val Ser Met Pro Gln Phe Arg Asp Phe Ala Ala Ala Ile Gly Met Asn
420 425 430

Val Gly Glu Lys Asp Ala Lys Asn Cys His Asp
435 440

<210> 70
<211> 455
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 70

Met Leu His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser Ser
1 5 10 15

Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser His
20 25 30

Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr
35 40 45

Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met Gln
50 55 60

Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile Asp
65 70 75 80

Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp Phe
85 90 95

Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly Val

100					105					110					
Tyr	Asp	Phe	Asp	Ser	Thr	Phe	Ile	Gly	Asp	Ala	Ser	Leu	Thr	Lys	Arg
	115						120					125			
Pro	Met	Gly	Arg	Val	Leu	Asn	Pro	Leu	Arg	Glu	Met	Gly	Val	Gln	Val
	130					135					140				
Lys	Ser	Glu	Asp	Gly	Asp	Arg	Leu	Pro	Val	Thr	Leu	Arg	Gly	Pro	Lys
145					150					155					160
Thr	Pro	Thr	Pro	Ile	Thr	Tyr	Arg	Val	Pro	Met	Ala	Ser	Ala	Gln	Val
				165					170					175	
Lys	Ser	Ala	Val	Leu	Leu	Ala	Gly	Leu	Asn	Thr	Pro	Gly	Ile	Thr	Thr
			180					185					190		
Val	Ile	Glu	Pro	Ile	Met	Thr	Arg	Asp	His	Thr	Glu	Lys	Met	Leu	Gln
	195						200					205			
Gly	Phe	Gly	Ala	Asn	Leu	Thr	Val	Glu	Thr	Asp	Ala	Asp	Gly	Val	Arg
	210					215					220				
Thr	Ile	Arg	Leu	Glu	Gly	Arg	Gly	Lys	Leu	Thr	Gly	Gln	Val	Ile	Asp
225					230					235					240
Val	Pro	Gly	Asp	Pro	Ser	Ser	Thr	Ala	Phe	Pro	Leu	Val	Ala	Ala	Leu
				245					250					255	
Leu	Val	Pro	Gly	Ser	Asp	Val	Thr	Ile	Leu	Asn	Val	Leu	Met	Asn	Pro
		260						265					270		
Thr	Arg	Thr	Gly	Leu	Ile	Leu	Thr	Leu	Gln	Glu	Met	Gly	Ala	Asp	Ile
	275						280					285			
Glu	Val	Ile	Asn	Pro	Arg	Leu	Ala	Gly	Gly	Glu	Asp	Val	Ala	Asp	Leu
	290					295					300				
Arg	Val	Arg	Ser	Ser	Thr	Leu	Lys	Gly	Val	Thr	Val	Pro	Glu	Asp	Arg
305					310					315					320
Ala	Pro	Ser	Met	Ile	Asp	Glu	Tyr	Pro	Ile	Leu	Ala	Val	Ala	Ala	Ala
				325					330					335	
Phe	Ala	Glu	Gly	Ala	Thr	Val	Met	Asn	Gly	Leu	Glu	Glu	Leu	Arg	Val
			340					345					350		
Lys	Glu	Ser	Asp	Arg	Leu	Ser	Ala	Val	Ala	Asn	Gly	Leu	Lys	Leu	Asn
	355						360					365			
Gly	Val	Asp	Cys	Asp	Glu	Gly	Glu	Thr	Ser	Leu	Val	Val	Arg	Gly	Arg
	370					375					380				
Pro	Asp	Gly	Lys	Gly	Leu	Gly	Asn	Ala	Ser	Gly	Ala	Ala	Val	Ala	Thr

186

7

385

390

395

400

His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Val
405 410 415

Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr Ser
420 425 430

Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile Glu
435 440 445

Leu Ser Asp Thr Lys Ala Ala
450 455

F1

cont.